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PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR PELLING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-16
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PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US09/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
PRIOR PRIOR DATE: 2000-01-05
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.9%;
Matches 1841; Conservative
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US-09-907-794A-118
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
1801 AGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCCAGCTCA 1842
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CURRENT FILING DATE: 2001-07-12
PRIOR PAPLICATION NUMBER: PCT/US00/04414
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-15
PRIOR PAPLICATION NUMBER: PCT/US99/21547
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1990-10-05
PRIOR PIL
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8-09-905-125A-118
; Sequence 118, Application US/09905125A
; Patent No. 6664376
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Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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Gao, Wei-Qiang
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APPLICANT:
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                                                                                                                                        Score 1840.4;
Pred. No. 0;
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0; Mismatches
                                                                                                                                        99.98;
                                                                                                                                        Query Match
Best Local Similarity 99.9
Matches 1841; Conservative
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 118
LENGTH: 1857
                                                                                 sapiens
                                                          ; TYPE: DNA
; ORGANISM: HOMO
US-09-905-125A-118
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APPLICANT: Tunas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, P. Mickey
APPLICANT: Wood, William, P. Mickey
APPLICANT: Wood, William, P. Mickey
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PELING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
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PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-18
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-29
PRIOR PLING DATE: 1999-10-21
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-10-05
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Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                       Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                     Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Matches 1841; Conservative
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SEQ ID NO 118
LENGTH: 1857
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; Sequence 118, Application US/09902775A
; GENERAL INFORMATION:
GAPPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Betefein, David
APPLICANT: Betefein, David
APPLICANT: Eaton, Dan L.
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        APPLICANTY: ROY, MATGROLAGE F.
APPLICANTY: ROY, MATGROLAGE F.
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APPLICANTY: TUMBAR: DITIOLAL
APPLICANTY: WOOD, WILLIAMS, DAILIE
APPLICANTY: WOOD, WILLIAMS, DAILIE
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCY: 1046-144
CURRENT APPLICATION NUMBER: 1050/906,700
CURRENT FILING DATE: 2000-09-18
FRIOR FILING DATE: 2000-09-18
FRIOR PELICATION NUMBER: 05 60/145,698
FRIOR PELICATION NUMBER: 05 60/146,222
FRIOR PELICATION NUMBER: PCT/US99/2054
FRIOR PELICATION NUMBER: PCT/US99/2054
FRIOR PELICATION NUMBER: PCT/US99/2054
FRIOR APPLICATION NUMBER: PCT/US99/2069
FRIOR APPLICATION NUMBER: PCT/US99/2109
FRIOR PELING DATE: 1999-0-1-5
FRIOR APPLICATION NUMBER: PCT/US99/28113
FRIOR APPLICATION NUMBER: PCT/US99/28113
FRIOR APPLICATION NUMBER: PCT/US99/28114
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Matches 1841; Conservative
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; ORGANISM: Homo sapiens
US-09-906-700-118
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Pred. No. 0;
0; Mismatches
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR PRLING DATE: 1999-07-28
PRIOR PRILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-30
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; ORGANISM: Homo sapiens
US-09-903-603A-118
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        1321 AGGTATCTTGAGCTTGGTTCTGGGCTCTTTCCTTGTGTACTGACGACCAGGCCAGCTGT 1380
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: GNE.1618P2C12
                                                                                                                                                                       TCCTTCCATCTCGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTGCCACTGGGATCC
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Patent No. 6767995
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Gerritsen, Mary E
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Paoni, Nicholas F
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Gao, Wei-Qiang
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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR PRILING DATE: 1999-11-29
PRIOR PRILING DATE: 1999-11-30
PRIOR PLILING DATE: 1999-12-02
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                                                                                                                                                                                                                  Length 1857;
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                                                                                                                                                                                                                  Score 1840.4;
Pred. No. 0;
0; Mismatches
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 118
LENGTH: 1857
                                                                                                                                                                                                                  99.98;
                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-909-064-118
                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                    Query Match
Best Local Simil
Matches 1841; (
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/09/909,064
PRIOR PRILOR DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-8
PRIOR FILING DATE: 1999-07-18
PRIOR FILING DATE: 1999-07-18
PRIOR FILING DATE: 1999-07-18
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/2814
PRIOR APPLICATION NUMBER: PCT/US99/2814
PRIOR APPLICATION NUMBER: PCT/US99/2856
PRIOR APPLICATION NUMBER: PCT/US99/2856
PRIOR APPLICATION NUMBER: PCT/US99/2856
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-07
PRIOR APPLICATION NUMBER: PCT/US99/3009
PRIOR APPLICATION NUMBER: PCT/US99/3009
PRIOR FILING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
    1741 GGAGAAACCCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTCCC 1800
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                                              AGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCA 1842
                                                                      AGCTGCTCAGGAGCCTGGCAACAAGAGAGAAAACTCCAGCTCA
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US-09-309-064-118
Sequence 118, Application US/0990964
; Patent No. 6818449
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Rahavin, Ivar J.
Pan, James
Paoni, Nicholas F.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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APPLICANT: Genemicech, Inc.
APPLICANT: Ashkenazi, Avii
APPLICANT: Botstein, David
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Eaton, Dan L.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/905,381A

CURRENT FILING DATE: 2001-07-13

PRIOR PRILOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-08

PRIOR FILING DATE: 1999-09-18

PRIOR FILING DATE: 1999-09-18

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1999-12-07

PRIOR PRIOR FILING DATE: 1999-12-07

PRIOR PRIOR FILING DATE: 1999-12-07

PRIOR PRIOR FILING DATE:
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Grimaldi, Christopher
Gurney, Austin L.
Hillan, Kenneth, J.
                   Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Tumas, Daniel
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Paoni, Nicholas F.
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Gerritsen, Mary E.
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Mather, Jennie P.
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Botstein, David
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                   AGTGCCCGAAGTGAAGGAGAATTCAAACAGACCTCGTCATTCCTGGTGTGAGCCTGGTCG
                                                               AGTGCCCGAAGTGAAGGAGAATTCAAACAGACCTCGTCATTCCTGGTGAGCCTGGTCG
                                                                                                             GCTCACCGCCTATCATCTGCATTTGCCTTACTCAGGTGCTACCGGACTCTGGCCCCTGAT
                                                                                                                                                           GCTCACCGCCTATCATCTGCATTTGCCTTACTCAGGTGCTACCGGACTCTGGCCCCTGAT
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Gaps ö Length 1857; Indels DB 4; 1; Score 1840.4; Pred. No. 0; 0; Mismatches 99.9%; ilarity 99.9%; Conservative C TYPE: DNA
CRGANISM: Homo sapiens
US-09-905-381A-118 Query Match Best Local Similarity Matches 1841; Conserv

RESULT 8
US-09-905-381A-118
US-09-905-381A-118
; Sequence 118, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi

420 420 480 480 540

900 600 999 999 720 720 780 780 840 840 900 900 960

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GAGGACCGGGTGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGAC 360
      AATCCTGTGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCCGTGTGGAGTGGAAG
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                                                                                                                    APPLICANT: Stewart, Timocny A.
APPLICANT: Thums, Daniel
APPLICANT: Thums, Daniel
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
CURRENT APPLICATION NUMBER: US/09/906,618
CURRENT FILING DATE: 1006-02-22
PRIOR FILING DATE: 1000-02-22
PRIOR PELING DATE: 1000-02-22
PRIOR PELING DATE: 1099-07-6
PRIOR PELING DATE: 1999-07-6
PRIOR PELING DATE: 1999-07-8
PRIOR PELING DATE: 1999-07-8
PRIOR PELING DATE: 1999-07-8
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PRIOR PELING DATE: 1999-07-18
PRIOR APPLICATION NUMBER: PCT/US99/2094
PRIOR PELING DATE: 1999-07-18
PRIOR APPLICATION NUMBER: PCT/US99/2091
PRIOR APPLICATION NUMBER: PCT/US99/2091
PRIOR PELING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/2091
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PRIOR APPLICATION NUMBER: PCT/US99/2091
PRIOR PELING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/2091
PRIOR PELING DATE: 1999-12-20
PRIOR PE
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Pred. No. 0;
0; Mismatches
                                                                                        Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Best Local Similarity 99.9
Matches 1841; Conservative
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US-09-906-618-118
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APPLICANT:
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APPLICANT: Kornecki, Malgorzata B.
TITLE OF INVENTION: Human Platelet F11 Receptor
FILE REFERENCE: 011.00221
CURRENT APPLICATION NUMBER: US/09/397,243D
CURRENT APPLICATION NUMBER: 60/100,638
PRIOR APPLICATION NUMBER: 60/100,638
PRIOR FILING DATE: 1998-09-16
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 0;
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; Patent No. 6699688
; GENERAL INFORMATION:
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Matches 1800; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 70
LENGTH: 1421
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ORGANISM: Human
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US-09-188-930-70
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                                                                                          TACACCTGGTTCAAAGATGGGATAGTGATGCCTACGAATCCCAAAAGCACCCGTGCCTTC
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GENERAL INFORMATION:
APPLICANT: Strachan, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Murison, James G.
APPLICANT: Murison, James G.
APPLICANT: Murison, James G.
APPLICANT: Murison, James G.
TITLE OF INVENTION: Compositions Isolated from Skir;
TITLE OF INVENTION: and Methods for Their Use
TITLE OF INVENTION: and Methods for Their Use
TITLE OF UNENT FILING DATE: 11999-05-14
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: PastSEQ for Windows Version 4.0
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99.3%; Pred. No. 0;
ive 6; Mismatches
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Patent No. 6573095
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Best Local Similarity 99.3
Matches 1350; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Mouse
US-09-312-283C-70
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Sequence 254, Application US/09312283C

Patent No. 65731095

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Sleeman, Matthew

APPLICANT: Onrust, Rene

APPLICANT: Kumble, Krishanand D.

TITLE OF INVENTION: Compositions Isolated from Skin Cells

TITLE OF INVENTION: and Methods for Their Use

TITLE REFERENCE: 11000.1011c2

CURRENT APPLICATION NUMBER: US/09/312,283C

CURRENT FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 425

SOFTWARE: EastSEQ for Windows Version 4.0

SEQ ID NO 254
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.6
Matches 1354; Conservative
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ORGANISM: Mouse
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APPLICANT: Murison, James Greg; TITLE OF INVENTION: Compositions Isolated Fro; TITLE OF INVENTION: and Methods For Their Use; FILE REFERENCE: 11000.1011c1 CURRENT APPLICATION NUMBER: US/09/188,930A; CURRENT FILING DATE: 1998-11-09; NUMBER OF SEQ ID NOS: 348; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 254
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  | 111 6.0 1131<br>111 6.0 1295   | 111 6.0 1131   | 111 6.0 1076   | 111 6.0 1022   | 6.0 1022   
   | 6.0 1022   | 111.6 6.1 65885  | 111.6 6.1 51917   | 111.8 6.1 32169   | 111.8 6.1 32169                                     | 111.8 6.1 1446  | 112 6.1 839  | 2 6.1 839   | 2 6.1 839  
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                                                                                                                                        <u>AAGGCGCAAGTCGAGAGAAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCC</u>
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                    Length 1842;
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                  Score 1840.4;
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Matches 1841; Conservative
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PC C12P21/02//C12P21/08, (C12N1/19,C12R1:645),(C12N1/21,C12R1:19),
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C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1842)
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60/066840 PI
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60/064103
60/064248
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60/059263
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/organism='Homo sapiens (human)'.
Location/Qualifiers
1801 AGCTGGTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCA 1842
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60/059113,17-SEP-1997 UG
60/059266,17-OCT-1997 UG
60/063286,17-OCT-1997 UG
60/063186,24-OCT-1997 UG
60/063120,24-OCT-1997 UG
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60/063124,28-OCT-1997 UG
60/063124,28-OCT-1997 UG
60/063134,29-OCT-1997 UG
60/063131,31-OCT-1997 UG
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60/066120,21-NOV-1997
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60/066453,25-NOV-1997
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GENEWTHOFH INC
OS HOMO sapiens (human)
PN JP 2002238586-A/98
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18-DEC-2001 JP 2001385205
17-SEP-1997 US 60/05911
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JP 2002238586-A/98.
Homo sapiens (human)
Homo sapiens
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18-SEP-1997 US
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PD 27-AUG-2
PF 18-DEC-2
PR 17-SEP-1
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C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10,
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60/066511 PR
60/066840 PI
,DIANE PENNICA,
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60/059283
60/062285
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Location/Qualifiers
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                                                                                                             - SEP - 1997
19997 US
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60/065846, 18-0CT-1997 UG
60/065846, 18-0CT-1997 UG
60/066772, 28-0CT-1997 UG
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60/059113,17-SEP-1997
60/059119,18-SEP-1997
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Pred. No. 0;
0; Mismatches
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OS Homo sapiens (human)
PN JP 2002238587-A/98
PP 18-DEC-2001 JP 2001385248
PR 17-SEP-1997 US 60/059115
               2002238587-A 98
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               Patent: JP
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1842)
Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and
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C12N5/10,

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FOR C12N5/10, C12R1:91), C12N1/19, C12N5/00, (C12N5/00, C12R1:19),

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FOR C12N5/10, C12R1:91), C12N15/10, C12N5/00, C12N1:19),

FOR C12N5/10, C12R1:191, CC

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FOR C12N5/10, C12R1:191, C12N15/10, C12N1/21, PC

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/organism='Homo sapiens (human)'.
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60/064215,29-OCT-1997 US 60
60/063870,03-NOV-1997 US 60
60/064809,12-NOV-1997 US 60
60/065846,18-NOV-1997 US 60
60/066120,21-NOV-1997 US 60
60/066770,24-NOV-1997 US 60
60/066770,24-NOV-1997 US 60
60/066453,25-NOV-1997 US 60
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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29-OCT-1997 US 60/06431

31-OCT-1997 US 60/06373

31-OCT-1997 US 60/06387

07-NOV-1997 US 60/06584

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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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ACCESSION

1201 AGGGATCAGGAATCCTGCATTGACTTCCTTCTAAGTAGTAGACACAAAAA 1260     1261 TGGCGGGGATCGCAGAATCCTGCACTTGACTTCCTTCTAAGTAGACACACAAAA 1220     1261 TGGCGGGGGTTCGCAGAAATCTCCACTGCCCACTGGCTGG	RESULT 7 AR410694 LOCUS Sequence 118 from patent US 6635468.  ACCESSION AR410694 VERSION AR410694 AR410694 AR410694 VERSION AR410694 AR410
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Patent: US 6686451-A 118 03-FEB-2004;
Location/Qualifiers
1. .1857
/organism="unknown"
/mol_type="genomic DNA"
                                                                                              Query Match
99.9%; Score 1840.4;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1841; Conservative 0; Mismatches
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In (bases 1 to 1857)

S Ashkenazi,A. Botstein,D., Desnoyers,L., Eaton,D.L., Ferrara,N.,
Filvaroff,E., Fong,S., Gao,W.-Q., Gerber,H., Gerritsen,M.E.,
Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Hillan,K.J.,
Kljavin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A.,
Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
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L Patent: US 6723535-A 118 20-APR-2004;
Location/Qualifiers

1. 1857

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Pred. No. 0;
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Best Local Similarity 99.9%;
Matches 1841; Conservative
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Crane test weight assembly and method

NAL Patent: US 672570-A 365 27-APR-2004;

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Location/Qualifiers

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                       1857 bp D
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Location/Qualifiers
1.1857
/organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                     Score 1840.4;
Pred. No. 0;
0; Mismatches
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US 6767995.
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                                                                                                                                                                                                                                           immune related
                                                                                                                                                         Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                     PAT
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                                                                                                     linear
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                      AGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCA
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                                                                                                     DNA
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Pred. No. 0;
0; Mismatches

    1857
    organism="Homo sapiens"
    mol type="unassigned DNA"
    db_xref="taxon:9606"

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                                                                                                    1857 bp
WO0119991.
                                                                                                                                                                                                                                                                            , Inc. (US)
Location/Qualifiers
                                                                                                             Sequence 5 from Patent AX098379
AX098379.1 GI:13537654
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Best Local Similarity 99.9%;
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1501   CTCTGCCTGTCCTCTGAATACAAGCTGACTTGACTGTGTCTGTGGAAAATGGG   1500	RESULT 15  AX454468  AX454468  BEGUNTION  Sequence 53 from Patent W00208284.  ACCESSION  AX454468.1 GI:21713858  AX454468.1 GI:21713858  Homo sapiens (human)  OKGANISM Homo sapiens  REFERENCE  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  REFERENCE  BACT.K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,  Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,  Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.  TITLE  Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis  JOURNAL Patent: W0 0208284-A 53 31-JAN-2002;  Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone (US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard, Hillan, Kenneth J. (US); Marsters, Scot A. (US); Pan, James (US); Paoni, Nicholas P. (US); Milliams, P. Mickey (US); Wood, William, Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William, Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William	in in d-d in-

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C1485 100.6 5.5 464 1 AV720671 AV720671 AV720671 AV720671 AV720671 AV720671 AV720671 AV720671 AV720671 AV78071			COMMENT 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime and enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.  FEATURES  Location/Qualifiers  Source  /organism="Homo sapiens" /mol Type="mRNA" /db xrefe="taxon:9606" /clone="CSODIO75YL24" /tissue type="Placenta Cot 25-normalized" /plasmid="pcMVSPORT_6" /plasmid="pcMVSPORT_6"	Query Match         83.4%;         Score 1535.4;         DB 3;         Length 1594;           Best Local Similarity         99.0%;         Pred. No. 0;         No. 0;         Adches 1558;         Conservative         0;         Mismatches         6;         Indels         9;         Gaps         1;           Qy         1         GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTCGGAGGGAG
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5.5 406 7 R12600 5.5 416 8 B91247 5.5 416 8 B91247 5.5 418 1 AA021061 5.5 442 8 AQ136592 5.5 481 1 AL704739 5.5 482 1 AL704739 5.5 496 1 AA705399 5.5 498 B AQ28474 5.5 524 B AQ38474 5.5 524 8 AQ28628 5.5 524 B AQ132425 5.5 557 5 BU948628 5.5 557 5 BU948628 5.5 573 2 AW162314	5.5 588 5 5.5 608 1 5.5 608 1 5.5 608 1 5.5 610 4 610 4 610 4 610 4 610 4 610 4 610 4 610 7 610 7 610 7 610 8 610	2307 8 2307 8 2307 8 2307 8 2307 8 2307 8 2307 8 2308 2 23		.5 1500 3 .5 1884 3 .6 2 343 8 .6 3 343 8 .6 4 405 2 .7 4 401 8 .8 4 421 7 .9 4 421 8 .9 4 421 8 .9 4 421 8 .9 4 432 8
C1412 C1413 C1413 1414 1415 1416 1416 1417 C1419 1420 1421 1421 1422 C1423 C1423 C1424 C1425 C1426 C1426 C1426 C1426 C1426 C1427 C14				

	REBULY 2  CR617300  CR61730  CR617300  CR61730	Query Match 80.0%; Score 1473.4; DB 3; Length 1514; Best Local Similarity 99.0%; Pred. No. 0; Matches 1496; Conservative 0; Mismatches 6; Indels 9; Gaps 1; I GTCTGTTCCCAGGAGTCCTTCGGGGGTGTTGTGTCAGGGGTGATGGGGACA 60
CTGGCATTGGGCAGTGTTACAGTGCACTCTGAACTCAGAATTCCTGAGAAT 180		TTTCCTACCACTGCTGAGTGGCCTGGAACTTGTTTAAAGTGTTTATTCCCCATTTCTTTG 1200

DB	RESULT 3  CREG08619  LOCUS  LOCUS  LOCUS  LOCUS  CREG0819  LOCUS  CREG0819  LOCUS  CREG0819  LOCUS  CREG0819  CREG08
	491   ACCATTGGGAACCGGCAGTGCTGACATGCTCAGACAGATGGTTCCCACCTTCTGAA   552     493   ACCATTGGGAACCGGGCAGTGCTGCTCCAGACAGATGGTTCCCCACCTTCTGAA   552     493   ACCATTGGGAACCGGGCAGTGCTGCTGCAGACAGACACAGATGCTCCCCACCTTCTGAA   552     494   ACCACTGGTTCAAAGATGGGATAGTGATGCCTACGAATCCCAAAAGACCCGTGCCTTC   610     553   TACACTGGTTCAAAGATGGGATAGTGATGCCTACGAATCCCAAAAGACCCCGTGCCTTC   611     611

1081   TCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCCATCCTCCTTCATGCCCTCCCT		1441 TCCTTCCATCTCTGGGGCCCACTCTTCTGTC 1428 TCCTTCCATCTCTCTGGGGCCCACTCTTTTTTTTTTTTT	AL549623 Homo sapiens PLACENTA COT 25-NORMALIZED Homo saclone CSODIO55YH06 5-PRIME, mRNA sequence. AL549623.3 GI:45750009 EST. Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Likaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom i (bases 1 to 1127) Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length, CDNA, libraries and normalization		n n o o
8 8 8 8 8	8 8 8 8 8	Oy  Db  Qy  Db  RESULT 4  RL549623	DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	COMMENT	FEATURES
ABLChes 1438; Conservative	181   AATCCTGTGAGGTGCTCTTCTGAACCTGAAGTCGGAATTCCTGAGAAT   225	Oy         361 ACTGGGACATACACTTGTATGGTCTCTGAGGAGGCGGCAACAGCTATGGGGAGGTCAAG         420           Db         406 ACTGGGACATACACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGAGGTCAAG         465           Cy         421 GTCAAGCTCATGGTGTTGTGCCTCCATCCAAGCTAACATCCCCTCTGCC         480           Db         466 GTCAAGCTCATCGTGCTTGTGCCTCCATCCAACACACACA	TACACCTGGTTCAAAGATGGGATAGTGATGCCTACGAATGCCCAAAAGCACCCGTGCCTTC 60	Oy         721 TCAAATGCTGTGCGCATGGAAGCTGTGGAGCGGAATGTGGGGGTCATCGTGGCCAGCCGTC         780           Db         766 TCAAATGCTGTGCGAAGCTGTGGGAATGTGGGGGGTCATCGTGGCAGCCGTC         825           Oy         781 CTTGTAACCCTGATTCTCCTGGGAATCTTGGTTTTTGGCATCTGGTTTGCCTATAGCCGA         840           Db         826 CTTGTAACCCTGATTCTCCTGGGAATCTTGGTTTTTGGCATCTGGTTTGCCTATAGCCGA         885           Qy         841 GCCACTTGACAGAACAAAGGAATCTTGGTTTTGGCATCTGGTTTGCCTATAGCCGA         885           Qy         841 GCCACTTTGACAGAACAAAAGAAAAGGAATCTTCGAGTAAGAAGGTGATTTACAGCCAGC	QY         901 AGTGCCCGAAGTGAAGGAGAATTCAAACAGACCTCGTCATTCCTGGTGTGAGCCTGGTCG         960           Db         900TAAGGAGAATTCAAACAGACCTCGTCATTCCTGGTGAGCCTGGTCG         960           QY         961 GCTCACCGCCTATCATCGCTTACTCAGGTGCTACCGGACTCTGGCCCTGAT         1020           Db         948 GCTCACCGCCTATCATCTGCCTTACTCAGGTGCTACCGGACTCTGGCCCCTGAT         1020           QY         1021 GTCTGTAGTTCACAGGATGCCTTATTTGTCTTCTACACCCCACAGGCCCCCTACTTCT         1080           CD         101 GTCTGTAGTTTCACAGGATGCCTTATTTGTCTTCTACACCCCACAGGGCCCCCTACTTCT         1080           CD         1008 GTCTGTAGTTTCACAGGATGCCTTATTTGTCTTCTACACCCCACAGGGCCCCCTACTTCT         1067

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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT & vector. Library
was normalized, Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                              ALS60725

ALS60725 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED Homo sapiens CDNA clone CSODL004YD03 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(Dases 1 to 993)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31284854.
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/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
25-NORMALIZED"
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For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODL004CB02QPl&c=250.r.
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; Pred. No. 2.1e-231;
12; Mismatches 9;
  GCTCA-CGCCTATAATCTGCTTTGCCTT 996
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/clone="C80DL004YD03"
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Matches 972; Conser
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                                                                                                 Length 1127;
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98.5%; Pred. No. 5.2e-232;
ive 7; Mismatches 5;
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                                                                                                                     Similarity
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                                                                                               Query Match
Best Local S:
Matches 973
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                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="texcn:9606"
/clone="CSODIOTSYL24"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
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primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
250.r
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                                                                For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS0DI075DF12NP1&c=250.r. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                       Length 1084;
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                                                                                                                                                                                                                                                                                                                                                       Score 926; DB 1; L
Pred. No. 4.4e-228;
3; Mismatches 9;
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2 rue Gaston Cremieux, CP 5766 - 91057 EVRY cedex - FRANCE
Email: sequeré@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSFORT 6 vector. Library
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AL576433 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI075YL24 3-PRIME, mRNA sequence.

AL576433.3 GI:46249298
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization (Dupublished (2001)
On Peb 16, 2001 this sequence version replaced gi:31314719. Contact: Genoscope
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                                      CACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATACACTTGTATGGTCTCTGAGGA
                                                                                      GCCTACAGTTAACATCCCCTCCTCTGCCACCATTGGGAACCGGGCAGTGCTGACATGCTC
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AGENCOURT_10034240 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6481188
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequefégenoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
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AL553289 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI075YL24 5-PRIME, mRNA sequence.
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1 (bases 1 to 1034)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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GCCCACCTGGCTGGCAGGGTCTTTGAATAGGTATCTTGAGCTTGGTTCTGGGCTCTTTC
                                                        CTTGTGTACTGACGACGACGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Feb 15, 2001 this sequence version replaced gi:31275103
Contact: Genoscope
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Pred. No. 3.6e-214;
1; Mismatches 19;
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/mol_type="mRNR"
/db zref="laxon:9606"
/clone="IMAGE=6480623"
/clone="IMAGE=6480623"
/tissue type="carcinoma, cell line"
/tasue type="carcinoma, cell line"
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/clone lib="NHH MGC_40"
/note="organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: BcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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I (bases 1 to 886)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Richard LLCW2660 row: k column: 24
High quality sequence stop: 698.
      547 TACACCTGGTTCAAAGATGGGATAGTGATGCCTACTAATCCCAAAAGCACCCGTGCCTTC
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/lab host="DH10B (phage-resistant)"
/lone_lib="NIH_MGC_40"
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Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into BcoRI/AhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
C California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Supperscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequenoring by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information of found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
High://image.llnl.gov
High quality sequence stop: 685.
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/db_xref="taxon:9606"
/clone="IMAGE:6481188"
                   Contact: Robert Strausberg, E
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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E 1 (bases 1 to 1020)

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Biosciance Corporation

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Llocation/Qualifiers
                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
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/clone="IMAGE:5740989"
   Homo sapiens (human)
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tch 46.7%; Score 859.6; DB 5; al Similarity 99.4%; Pred. No. 6.4e-211; 862; Conservative 0; Mismatches 5;
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/lab\_host="DH10B (phage-resistant)"
/clone\_lib="NIH\_MGC\_88"
/note="lorgan: small intestine; Vector: pCMV-SPORT6;
Site\_l: NotI; Site\_2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size 1:76; kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH\_MGC Library." TCATATTGGCGATCCTGTTGTGCTCCCTGGCATTGGGCAGTGTTACAGTGCACTCTTCTG AACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGATGGGATAGTGATGCCTA TCAGTGGCCTGATCGCGATGGGGACAAAGGCGCAAGTCGAGGAGAAACTGTTGTGCCTCT 95 TCATATTGGCGATCCTGTTGTGCTCCTGGCATTGGGCAGTGTTACAGTGCACTCTTCTG 155 AACCTGAAGTCCAGAATTCCTGAGAATAATCCTGTGAAGTTGTCCTGTGCCTACTCGGGCT 275 ATAATAACAAGATCACAGCTTCCTATGAGGACCGGGTGACCTTCTTGCCAACTGGTATCA CCTTCAAGTCCGTGACACGGGAAGACACTGGGACATACACTTGTATGGTCTCTGAGGAAG cracagriraacarccccrccrcrcccaccarriggaaccgggcagrgcrcargcrcag TCAGTGGCCTGATCGCGATGGGGACAAAGGCGCAAGTCGAGAGAAACTGTTGTGCCTCT 215 TTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCAAGGAGACACCACCAGCAGTCGTTTGCT 181 TITCIICICCCCGIGIGGAGIGGAAGIITGACCAAGGAGACACCACCAGACICGIITGCI CTACAGTTAACATCCCCTCCTCTGCCACCATTGGGAACCGGGCAGTGCTGACATGCTCAG Gapa ö 46.3%; Score 853.4; DB 4; Length 1020; 99.1%; Pred. No. 2.6e-209; tive 0; Mismatches 8; Indels 0; Matches 857; Conservative 455 421 515 원 : 상 셤 ઠે

DEFINITION

ACCESSION VERSION KEYWORDS

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BX372242 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED Homo sapiens clone CSODL004YD03 3-PRIME, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                    GECTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTCAGTGGCCTGATCGCGATGGGGAACA
                                                                                                                                                                                          CTGGCATTGGGCAGTGTTACAGTGCACTCTTCTGAACCTGAAGTCAGAATTCCTGAGAAT
                                                                                                                                  AAGGCGCAAGTYGAGAAGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCC
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Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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//cissue Vtye="PIACBNTA COT 25-NORWALIZED"
//clone lib="Homo sapiens PIACENTA COT 25-NORWALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
/note="lst strand cDNA was primed with a NotI-oligo(dT)
/rimer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EORR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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1 (bases 1 to 896)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                          CGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCTGAATCCCACAAGAG
AACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGATGGGATAGTGATGCCTA
                                  CGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCTGAATCCCACAACAG
                                                                                                              GAGAGCTGGTCTTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACAGCTGTGAGGCAC
                                                                                                                                GAGAGCTGGTCTTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACAGCTGTGAGGAC
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Pred. No. 1.4e-206;
1; Mismatches 3;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Best Local Similarity 99.5%;
Matches 844; Conservative 1
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
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into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                          GTGTTTATTCCCCATTTCTTTGAGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTC 1238
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                     CCCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCCCAT 1118
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/mol type="mana"
/db xref="taxon:9606"
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/clone=Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone=Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note=Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note=Tib="taxon cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTGACGACCAGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCGGAAA 1415
                                                                                                                                                         CCTCCTTCATGCCCTCCCTCTTTCCTACCACTGCTGAGTGGCCTGGAACTTGTTTAAA
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                                                                                     CCCCACAGGGCCCCCTACTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCCAT
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31271416.
Contact: Genoscope
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94.0%; Pred. No. 2.3e-203;
tive 13; Mismatches 37;
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                                                                                                                                                                                                           Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Email: segrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAI042ZDII_CS04020_1&c=250.r. Location/Qualifiers
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/db_xref="taxon:9606"
/clone="CSOLO04YD03"
/cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
/cell_lihe="RAMOS CELL LINE"
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Mammalia; Eutheria; Primates; Catarrhini; Hor
1 (bases 1 to 907)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Pred. No. 1.2e-205;
0; Mismatches 23;
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Vertebrata; Euteleostomi;

Catarrhini; Hominidae; Homo.

Eukaryota; Metazoa; Chordata; Craniata; Verte Mammalia; Eutheria; Primates; Catarrhini; Hor 1. (bases 1 to 925) Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Pull-length cDNA libraries and normalization Unpublished (2001)

GI:30307616

BX327155 BX327155.1

Homo sapiens (human)

Homo sapiens

Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Genoscope - Centre Centre S. 2 rue Gaston Cremieux, CP 5706 - 91057 EWRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
ist strand cDNA was primed with a Not1-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and Ecok V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster

250.r For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS0BAF024ZF12\_AF02303\_2&c=250.r. Location/Qualifiers

/organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606"

us-10-785-220b-11.rst

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/clone="CSODIO32YCO2"
/tissue type="PLACENYA COT 25-NORMALIZED"
/tissue type="PLACENYA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENYA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.'
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BX327155 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI032YC02 5-PRIME, mRNA sequence.

RESULT 14 BX327155 LOCUS DEFINITION

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B I (bases 1 to 907)

S NIH-MCC http://mgc.nci.nih.gov/.

I Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

High quality sequence stop: 692.

High quality sequence stop: 692.
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AGENCOURT 10039280 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6480422
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/clone_lib="NH1 MGC 40"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXkhoI sites using the following 5: adaptor: GGCACGAG(G). Library constructed
                            AATAGGTATCTTGAGCTTGGTTCTGGGCTCTTTCCTTGTGTACTGACGACCAGGGCCAGC
                                                                                                                                                           GGGTCCTTCCATCTCTGGGCCCCACTCTCTCTGTCTT - CCATGGGGAGTGCCACTGGGA
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                                                                                                                                                                                                                                                            ATGGGAGCTCTTGTTGTGGAGCATAG-TAAATTTTCAGAGAACTTGAAGCCAAAAGGA
                                                                                                                                                                                                                                                                                                                    TTTAAAACCGCTGCTCTAAAGAAAAGAAAACTGGAGGC-TGGGCGCAGTGGCTCACGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6480422"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BQ928239.1 GI:22343270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
Homo sapiens
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BQ928239
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BQ928239
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                1;
                                                                                                                                                Length 907
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                                                                                                                                              Score 803.2; DB 5;
Pred. No. 2.5e-196;
0; Mismatches 13;
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AASO0159 standard; cDNA; 1857 BP.
Human cDNA clone DNA40628-1216 encoding PRO301 (UNQ264)
WO200119991-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS21426 standard; cDNA; 1857 BP.
Human cDNA sequence encoding for PRO301 polypeptide
WO200140466-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC97460 standard; cDNA; 1857 BP.
Human angiogenesis-associated protein PRO301 cDNA,
WO200053753-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of human polypeptide PRO301.72-DRC-2000.77037-A2.72-DRC-2000.77037-A2.72-DRC-2000.77037-A2.72-DRC-2000.77037-A2.72-DRC-2000.77037-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770-A2.770
                Score 1840.4;
Pred. No. 0;
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(GETH ) GENENTECH INC.
17 Match 99.9%; Score 1840.4;
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Human PRO301 cDNA sequence SEQ ID NO:53.
WO200200690-A2.
                                                                              AAA49723 standard; cDNA; 1857 BP.
Human PRO301 cDNA clone DNA40628-1216.
WO200037638-A2.
29-UDN-2000.
                                                                                                                                                                                                                                                          ADC78438 standard; cDNA; 1857 BP.
Human PRO301 cDNA.
WO200015796-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF72393 standard; cDNA; 1857 BP.
Human PRO301 cDNA.
WO200104311-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 13
                                Best Local Similarity RESULT 6
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(GETH ) GENI
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GenCore version 5.1.6
September 8, 2005, 10:59:16; Search time 1032 Seconds (without alignments)
10566.050 Million cell updates/sec
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                                                                                                                                             Sequence:
Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0
Searched:
Searched: 4390.206 seqge, 2559870667 residues
Total number of hits satisfying chosen parameters: 8780412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12; Length 1856;
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(GETH ) GENENTECH INC.
2ry Match 99.9%; Score 1840.4;
2ry Match 99.9%; Pred. No. 0;
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Pred. No. 0;
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Human PRO301 protein encoding cDNA, UNQ264.
WO200015797-A2.
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Pred. No. 0;
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Human secreted/transmembrane protein cDNA,
US2004137561-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX37714 standard; DNA; 1842 BP.
Human cDNA clone DNA40628 encoding PRO301
WO9914241-A2.
                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
Database : N_Geneseq_16Dec04:*
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Protein PRO301 cDNA clone DNA40628-1216.
WO9914328-A2.
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Human PRO301 cDNA sequence SEQ ID NO:89.
008-UNN-2000
GG-TUN-2000.
(GETH ) GENENTECH INC.
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25-MAR-1999.
(GETH ) GENENTECH INC.
"atch 99.9%; SC
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25-MAR-1999.
(GETH ) GENENTECH INC.
""+Ch 99.9%;
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Maximum DB seq length: 200000000
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2004.
2.674 GENENTECH II.
2.677 MATCh
Best Local Similarity 5
RESULT.4
ID AAZ52204 standar
DE Human PRO30°
PN WO20017
PD 23-7°
PA
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(GETH ) GENENTECH INC.
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Best Local Similarity
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NO:118

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SEQ

Length 1857;

DB 4;

Length 1857;

DB 6;

Length 1857;

4;

<u>D</u>B

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RESULT 23
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Pred. No. 0;
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DNA encoding novel secreted and transmembrane protein PRO301 US2003017563-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2002197671-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003032063-A1.
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Wham cDNA encoding secreted/transmembrane protein PRO301
US2002132240-A1.
                                                                                                                                                                                                                                                          Human cDNA for secreted/transmembrane protein PRO301.
US2003003530-A1.
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26-DEC-2002.
(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
(GETH ) GENENTECH 1840.4;
(GETH ) 99.9%; Pred. No. 0;
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CDNA encoding human PRO polypeptide #183
20-FEB-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                              ACA60097 standard; cDNA; 1857 BP
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02-JAN-2003.
(GETH ) GENENTECH INC.
09.9%;
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99.98;
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(GDDD/) GODDARD A.
(GDDV) GODOWSKI P J.
(GURN/) GURNEY A L.
(HILL) HILLAN K J.
(MARS/) MARSTERS S A.
(PANJ/) PAN J.
(PANJ/) PAN J.
(STEP/) STEPHAN J F.
(STEP/) STEPHAN J F.
(WILL/) WILLIAMS P M.
            GERBER H.
GERRITSEN M E.
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JAJA1.

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JH ) GENENTECH 1.

Jest Match
Best Local Similarity PRESULT 17
ID ACA03785 stander
DE CDNA encodir
PN US20030**
PD 20-7
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Ser Local Similarity >> RESULT 18

ID ABX71545 stand*

DE Human cDNA

PN US20021*

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RESULT 19
ID ACA4985 standard; CD
DE Novel human secreted
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC
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Best Local Similarity
RESULT 16
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RESULT 15
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Human cDNA encoding a secreted/transmembrane protein, SEQ ID 365.
US2003032155-A1.
13-FEB-2003.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2002177165-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003017463-A1.
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Novel human secreted and transmembrane protein PRO301 DNA US2003032062-A1.
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Human cDNA encoding secreted/transmembrane protein PRO301
US2003032057-A1.
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Human secreted / transmembrane polypeptide PRO301 cDNA
US2003036060-A1.
ACD41977 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein (PRO) cDNA #183.
US2003036179-A1.
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Human secreted/transmembrane protein cDNA, #23
US2002160374-A1.
                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding human secreted protein PRO301.
US2003023054-A1.
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CO-FEB-2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
ery Match 99.9%; Pred. No. 0;
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Pred. No. 0;
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31-007-2002.
(GETH ) GENENTECH INC.
99.9%;
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13-PEB-2003.
(GETH ) GENENTECH INC.
"MATCh "1" tty 99.9%;
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30-JAN-2003.
(GETH ) GENENTECH INC.
Match '...ttv 99.9%;
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20-FBB-2003.
(GETH ) GENENTECH INC.
99.9%;
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13-FSB-2003.
(GETH ) GENENTECH INC.
99.9%;
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99.98;
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23-JAN-2003.
(GETH ) GENENTECH INC.
99.9%;
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Best Local Similarity 99.9%;
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(GETH ) GENENTECH INC.
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Best Local Similarity
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Best Local Similarity
RESULT 26
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RESULT 27
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Length 1857;
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(GETH ) GENENTECH INC.
ery Match 99.9%; Score 1840.4; DB 9; Length 1857;
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003082693-Al.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003087345-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACU66887 standard; CDNA; 1857 BP.
Human CDNA encoding secreted/transmembrane protein PRO301.
052003045693-A1.
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                                                                             DB
                                                                                                                                                                                                                                                                                                                                                              Human secreted/transmembrane protein cDNA, #25.
US2003039971-A1.
27-FEB-2003.
(GETH ) GENENTECH INC. 99.9%; Score 1840.4; DB
st Local Similarity 99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                  Score 1840.4;
Pred. No. 0;
                                                                          Score 1840.4;
Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADB30545 standard; cDNA; 1857 BP.
cDNA encoding human PRO polypeptide #183.
US2003068794-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PRO polynucleotide #183.
US2003068795-A1.
                                                                                                                                           ADA47743 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003073215-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADA97053 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003082705-A1.
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Human PRO polynucleotide #183.
US2003082763-A1.
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17-APR-2003.
(GETH ) GENENTECH INC.
99.9%;
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06-MAR-2003.
(GETH ) GENENTECH INC.
MATCh "Twity 99.9%;
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10-ARR-2003.
(GETH ) GENENTECH INC.
99.9%;
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01-MAY-2003.
(GETH ) GENENTECH INC.
99.9%;
                           08-MAY-2003.
1 (GETH) GENENTECH INC.
Query Match 99.9%;
Best Local Similarity 99.9%;
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(GETH ) GENENTECH INC.
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J4-A1.

J5-A31.

J6-A1.

J6-A1.

J7-A1.

J7-A1
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Best Local Similarity
RESULT 44
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Best Local Similarity
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       US2003087350-A1.
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PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1840.4; DB 9; Length 1857;
Best Local Similarity 99.9%; Pred. No. 0;
                                                                                                   Length 1857;
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003022328-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003068796-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003082711-A1.
Human secreted / transmembrane polypeptide PRO301 cDNA.
US2003027143-A1.
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(GETH ) GENENTECH INC.
17 Match 99.9%; Score 1840.4;
27 Match 99.9%; Pred. No. 0;
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13-MAR-2003.
(GETH) GENENTECH INC.
(GETH) 99.9%; Score 1840.4;

PER 99.9%; Pred. No. 0;
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No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Human secreted/transmembrane protein cDNA,
US2003092002-A1.
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CDNA encoding human PRO polypeptide #183.
US2003082704-A1.
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Pred. 1
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Human PRO polynucleotide #183.
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06-FEB-2003.
(GETH ) GENENTECH INC.
Warch 99.9%; Sr
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17-APR-2003.
(GETH ) GENENTECH INC.
99.9%;
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10-APR-2003.
(GETH ) GENENTECH INC.
99.9%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                    wuery Match
Best Local Similarity
RESULT 32
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RESULT 35
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RESULT 40
ID ADB15957 standard;
DE Human PRO polynucle
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Best Local Similarity
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US2003049816-A1.
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Query Match

A B B B B B

Query Match

Query Match

RESULT 37

Query Match

Query Match

RESULT 39

BARA

RESULT 38

A D D D D

Query Match

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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 61
ID ADA74491 standard; cl
DE Human PRO polynucleo'
PN US2003068798-A1.
PD 10-ARR-2003.
PA (GETH ) GENENTECH IN
                                                                                                                         Query Match
Best Local Similarity
RESULT 60
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                    Query Match
Best Local Similarity
RESULT 59
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                                  DB 9; Length 1857;
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003073211-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003082691-A1.
01-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                   ADA91790 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA
US2003082694-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted/transmembrane polypeptide PRO301 cDNA US2003044844-A1.
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08-MAY-2003.
(GETH ) GENENTECH INC.
Hery Match 99.9%; Score 1840.4;
                                                                                                   99.9%; Score 1840.4; 99.9%; Pred. No. 0;
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24-APR-2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
ery Match 99.9%; Pred. No. 0;
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OG-MAR-2003.

(GETH ) GENENTECH INC.

199.9%; Score 1840.4;

191.9%; Pred. No. 0;
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                           Human secreted/transmembrane protein cDNA, US2003049621-A1.
                                                                    ADB16698 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003087349-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA94029 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003077722-A1.
                                                                                                                                                                          ACD83048 standard; cDNA; 1857 BP. Human PRO polynucleotide #21. 052003044793-A1. 06-MAR-2003.
                                                                                                                                                                                                                                                                                 ADA16154 standard; cDNA; 1857 BP.
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Human PRO polynucleotide #183.
US2003087351-A1.
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Best Local Similarity 9
RESULT 54
ID ADB14853 stands
DE Human PRO C
PN US2030
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity 5
RESULT 58
ID ADB19925 standard; CDP
DE Novel human secreted 6
PN W22003082691-A1.
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Best Local Similarity
RESULT 57
                                Query Match
Best Local Similarity
RESULT 50
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Best Local Similarity
RESULT 56
                                                                                                                                             Best Local Similarity
RESULT 51
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DB 9; Length 1857;
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 Length 1857;
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Novel human secreted and transmembrane protein PRO301 cDNA.
01-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                ACD98606 standard; cDNA; 1857 BP. Novel human secreted and transmembrane protein PRO301 cDNA. US2003044945-Al.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003082695-Al.
   DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADA42299 standard; cDNa; 1857 BP.
Human secreted/transmembrane protein cDNA, #25.
US2003054401-A1.
                                                                                                                                                                                                                                                                                                                                                                                                    10-APR-2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
99.9%; Pred. No. 0;
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Pred. No. 0;
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(GETH ) GENENTECH INC.
199.9%; Score 1840.4;
ry Match 99.9%; Pred. No. 0;
99.9%; Score 1840.4; 99.9%; Pred. No. 0;
                                                                                                                                               Score 1840.4;
Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Human PRO polynucleotide SEQ ID NO 365.
US2003077713-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADA75211 standard; cDNA; 1857 BP. Human PRO polynucleotide #183. US2003073216-A1. 17-APR-2003. (GETH) GENEWTECH INC. 99.9%; Score 20est Local Similarity 99.9%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA82248 standard; cDNA; 1857 BP. Human PRO polynucleotide #183. 01-82003082701-A1. (GETH) GENENTECH INC.
                                                    ADB13237 standard, cDNA, 1857 BP.
Human PRO polynucleotide #183.
US2003082710-A1.
                                                                                                                                                                                                                                                                                                                                               ADA74491 standard; cDNA; 1857 BP. Human PRO polynucleotide #183. US2003068798-Al.
                                                                                              USZUCZCZ
01-MAY-2003.
(GETH ) GENENTECH INC.
MATCh ''. MATCh ''. MATCh ''.
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06-MAR-2003.

(GETH ) GENENTECH INC.

99.9%;
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20-MR-2003.
(GETH ) GENENTECH INC.
99.9%;
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01-MAY-2003.
(GETH) GENENTECH INC.
MATCh --1 arity 99.9%;
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Best Local Similarity
                    RESULT
99.9%; Score 1840.4; DB 9; Length 1857; 99.9%; Pred. No. 0;
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CDNA encoding human PRO polypeptide #183.

US203095386-A1.

22-MAY-2003.

(GETH ) GENENTECH INC.

99.9%; Score 1840.4; DB 9; Length 1857;
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JENENTECH INC.

JENENTECH INC.

SHEST JOCAL SIMILARITY 99.9%; SCOTE 1840.4; DB RESULT 76

ID ADB31097 standard; CDNA; 1857 RP

DE CDNA encoding human PRO TRY US2003096386-A1

PD 22-MAY-2017

PA //T
                                                                                         USZUCZON

03-APR-2003.

(GETH ) GENENTECH INC.

99.9%; Score 1840.4;

PETY NAICH 99.9%; Pred. No. 0;
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PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 99.9%; Pred. No. 0;

RESULT 74
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24-ARR-2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
ery Match 99.9%; Pred. No. 0;
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                                                                                                                                                                                        ADB29993 standard; cDNA; 1857 BP.
CDNA encoding human PRO polypeptide #183.
US2003073214-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADB25284 standard; cDNA; 1857 BP.
Human PRO polynucleotide SEQ ID NO 365.
US2003077715-A1.
                                                 ACD23226 standard; cDNA; 1857 BP.
Human PRO polynucleotide #21.
US2003064367-A1.
                                                                                                                                                                                                                                                                                                                                     ADA80521 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003082761-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADA75763 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003082703-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA46988 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003073210-A1.
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Human PRO polynucleotide #183.
US2003077721-A1.
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(GETH) GENENTECH IN

Query Match
Best Local Similarity 9.

RESULT 70

ID ADA80521 stand?

DE Human PRO r

PN US2003"

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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 75
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                                                                                                                                                   Best Local Similarity RESULT 69
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                Local Similarity
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01-MAY-2003,
(GETH ) GENENTECH INC.
ery Match 99.9%; Score 1840.4; DB 9; Length 1857;
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Novel human secreted and transmembrane protein PRO301 CDNA.
                               ADAblue.
Homo sapiens.
10 13-MAR-2003.
D 13-MAR-2003.
PA (GETH ) GENENTECH INC.
99.9%; Score 1840.4; DB
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PA (GETH ) GENENTECH INC.
Query Match 99.9%; Score 1840.4;
Best Local Similarity 99.9%; Pred. No. 0;
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(GETH ) GENENTECH INC.
Sry Match 99.9%; Score 1840.4;
Sry Match 99.9%; Pred. No. 0;
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01-MAY-2003.
(GFTH) GENENTECH INC.
199.9%; Score 1840.4;
1ery Match 99.9%; Pred. No. 0;
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10-APR-2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
ery Match 99.9%; Pred. No. 0;
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99.9%; Pred. No. 0;
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US2003082760-A1.
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cDNA encoding human PRO polypeptide #183.
US2003077710-A1.
                                                                                                                                                                         ADB34172 standard; cDNA; 1857 BP.
Human PRO polynucleotide SEQ ID NO 365.
US2003077714-Al.
                                                                                                                                                                                                                                                                                                                        ADA96501 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003082690-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA81073 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003082702-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADA95949 standard; cDNA; 1857 BP. Human PRO polynucleotide #183. 02003003062759-Al. 01-MAY-2003. (GETH ) GENENTECH INC.
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US2003068797-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                   Best Local Similarity RESULT 78
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RESULT 82
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Best Local Similarity
RESULT 85
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Best Local Similarity
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Length 1857;
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                                                                                     Length 1857;
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          ADA86945 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003082709-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADA46436 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003054516-A1.
20-MAR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADA88048 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003082700-A1.
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                                                                                                                                                                                                         DB 9;
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CU3082540-Al.

CU 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 99.9%; Score 1840.4; DB
RESULT 90

ID ADA88048 standard; CDNA, 1857 BP
DE Novel human secreted and PN US2003082700-Al.

PD 01-MAY-200.
                                                                                                                                              #25.
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                                                                                     DB
                                                                                                                                                                                                                                                                 Human secreted/transmembrane protein cDNA, #25.
US2003049622-A1.
                                                                                                                                                                                                                                                                                                                                                                                     Human secreted/transmembrane protein cDNA, #25. US2003082540-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) 01-MAY-2003.

(GETH) GENENTECH INC.

Query Match 99.9%; Score 1840.4;

Best Local Similarity 99.9%; Pred. No. 0;
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Best Local Similarity 99.9%; Pred. No. 0;
RESULT 94
                                                                                                                                             Human secreted/transmembrane protein cDNA, US2003039969-A1.
27-FEB-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                       Score 1840.4;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                     Query Match 99.9%; Score 1840.4; Best Local Similarity 99.9%; Pred. No. 0; RESULT 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1840.4;
Pred. No. 0;
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Human secreted/transmembrane protein cDNA,
US2003017498-A1.
                                                                                  99.9%; Score 1840.4; 99.9%; Pred. No. 0;
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CDNA encoding human PRO polypeptide #183.
01-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                      Leary Match
Best Local Similarity 99.9%; Sct.
RESULT 88
ID ADA13007 standard; CDN*
DE Human secreted/tr-
PN US2003049607
PD 13-Mar
                                                                                                                                                                                                                                                   ADA13007 standard; cDNA; 1857 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA42725 standard; cDNA; 1857 BP.
                                                                                                                               ADA16578 standard; cDNA; 1857 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.9%;
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                              USICOLO 23-JAN-2003.
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(GETH ) GENENTECH INC.
                                                                       (GETH ) GENENTECH INC.
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Best Local S
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ID ADA46
DE NOVE]
PN US200
PD 20-M2
RESULT 86
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99.9%; Score 1840.4; DB 9; Length 1857; 99.9%; Pred. No. 0;
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                                                                                          Length 1857;
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                                                                                                                                                                                                                                                                                       ADA88600 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA. US2003073213-A1.
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US2003087344-Al.
08-MAY-2003.
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SULT 102
) ACD2388 standard; CDNA; LUN US2003664923-A1.
N US2003664923-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
PA (GETH ) GENENTECH INC.
199.9%; Score 1840.4; DB
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17-APR-2003.
17-APR-2003.
16TH ) GENENTECH INC.
99.9%; Score 1840.4;
99.9%; Pred. No. 0;
                                                    01-MAY-2003.
(GETH ) GENENTECH INC.
17 Match 99.9%; Score 1840.4;
17 Match 99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human PRO polynucleotide #183.
US2003082686-A1.
01-MAY-2003.
G-FM H GENENTECH INC.
PRY Match 99.9%; Score 1840.4; St Local Similarity 99.9%; Pred. No. 0;
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                                                                                                                                                                                                                                    Score 1840.4;
Pred. No. 0;
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ADB29018 standard; cDNA; 1857 BP.
CDNA encoding human PRO polypeptide #183.
US2003082706-Al.
01-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding human PRO polypeptide #183. US2003022239-A1.
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ID ADA66986 standard; cDNA; 1857 BP. DE Human PRO polynucleotide #183. PD 10-APR-2003.

PD (GETH) GENENTECH INC.
                                                                                                                              Luman PRO polynucleotide #183.
US2003059909-Al.
27-MAR-1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA; 1857 BP.
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27-MRR-2003.
(GETH ) GENENTECH INC.
MATCh 'TTHV 99.9%;
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(GETH ) GENENTECH INC.
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RESULT 101
ID ACD30262 standard; cl
DE Human cDNA encoding i
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC
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Best Local Similarity
RESULT 97
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RESULT 99
ID ADB27362 standard,
DE CDNA encoding human
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                                                                                                   Best Local Similarity RESULT 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA97605 standard;
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Length 1857;

Length 1857;

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Length 1857;

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Length 1857;

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DB 10; Length 1857;
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                                                                                             DB 10; Length 1857;
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003082764-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA
01.2830.00.02867-A1.
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Pred. No. 0;
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24-APR-2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
erv Match 99.9%; Pred. No. 0;
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Human secreted/transmembrane protein cDNA,
US2003082542-A1.
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Human PRO polynucleotide SEQ ID NO 365.
US2003077717-A1.
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Human PRO polynucleotide SEQ ID NO 365.
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) GENENTECH INC.
99.9%; Sr
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US2003082697-A1.
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24-APR-2003.
(GETH ) GENENTECH INC.
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01-MRY-2003.
(GETH ) GENENTECH INC.
99.9%;
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Local Similarity 99.9%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 115
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Best Local Similarity
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(GETH) GENENTECH INC.
ry Match
1999; Score 1840.4; DB 9; Length 1857;
1700 Similarity 99.9%; Pred. No. 0;
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Novel human secreted and transmembrane protein PRO301 cDNA, 01.200308212-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003082766-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003087347-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003082689-A1.
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Human secreted/transmembrane protein cDNA, #25.
US2003077654-A1.
24-APR-2003.
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(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
ery Match 99.9%; Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Human PRO polynucleotide SEQ ID NO 365.
US2003077712-A1.
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Human PRO polynucleotide #183.
US2003082698-A1.
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Human PRO polynucleotide #183.
US2003082762-A1.
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24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 99.9%; Pre
RESULT 105
ID ADB23620 standard; CDW
DE Human PRO polynur'
PN US200307771°
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US2003087352-A1.
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01.MAY-2003.
(GETH ) GENENTECH INC.
99.9%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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July Match Best Local Similarity PRESULT 112

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(GETH ) GENENTECH INC
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Best Local Similarity
RESULT 109
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RESULT 107
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Best Local Similarity
RESULT 108
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RESULT 113
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Length 1857;

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13-MAR.2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4; DB 10; Length 1857;
  DB 10; Length 1857;
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                                                                                                                                                  ADB46533 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003082692-A1.
                                                                                                             DB 10;
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Human secreted/transmembrane protein cDNA, #25.
US2003059828-Al.
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  Score 1840.4;
Pred. No. 0;
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No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Human secreted/transmembrane protein cDNA, US2003036094-A1.
30-FEB-2003.
(GETH ) GENENTECH INC.
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Pred. No. 0;
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Pred. No. 0;
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Human secreted/transmembrane protein cDNA,
US2003059772-A1.
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Human secreted/transmembrane protein cDNA,
US2003036061-A1.
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Pred. No. 0;
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                                      ADB36138 standard; cDNA; 1857 BP.
Human PRO polynucleotide SEQ ID NO 365.
US2003077720-A1.
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Pred.
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01-MAY-2003.
(GETH ) GENENTECH INC.
Watch 99.9%; Sc
                                                                  US20030.
24-APR-2003.
(GETH ) GENENTECH INC.
99.9%;
  99.9<del>8</del>;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
Ouery Match
RESULT 123
ID ADB36138 standard; ch
DE Human PRO polynucleot
PD 24-ARR-2003.
PD 24-ARR-2003.
PA (GETH ) GENENTECH INC
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Best Local Similarity
RESULT 125
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Best Local Similarity
RESULT 131
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Best Local Similarity
RESULT 124
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RESULT 130
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RESULT 127
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RESULT 126
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Length 1857;
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Novel human secreted and transmembrane protein cDNA Seq ID365.
US2003087365-A1.
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Novel human secreted and transmembrane protein cDNA Seg ID365.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003092106-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human secreted and transmembrane protein PRO301 cDNA US2003092107-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUC59932 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA
                                                                                  Human secreted/transmembrane protein cDNA, #25.
US2003054400-A1.
CD-MAR-2003.
(GETH) GENENTECH INC.
199.9%; Score 1840.4; DB 10; St Local Similarity 99.9%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                           Human secreted/transmembrane protein cDNA, #25.
US2003054441-A1.
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15-MAY-2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
lery Match 99.9%; Pred. No. 0;
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No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Best Local Similarity 99.9%; Score 1840.4;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 135
DE Human Secreted/transmembrane protein CDNA,
PN US2003073079-A1.
PD 17-APR-2003
PA (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1840.4;
Pred. No. 0;
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Best Local Similarity 99.9%; Pred. No. 0; RESULT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 0;
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Pred.
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                                                              CDNA; 1857 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADC33840 standard; cDNA; 1857 BP
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17-APR-2003.
(GETH ) GENENTECH INC.
99.9%;
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20-MRR-2003.
(GETH ) GENENTECH INC.
99.9%;
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15-WX-2003.
(GETH ) GENENTECH INC.
99.9%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
RESULT 134
ID ADC33840 standard; cl
DE Human secreted/transn
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC
                                                                                                                                                                                                                      Best Local Similarity
RESULT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
RESULT 139
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Best Local Similarity
                                                         ADC40735 standard;
                                                                                                                                                                                                                                                                                     ADC19392 standard;
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RESULT 138
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Length 1857;

DB 10;

Length 1857;

DB 10;

DB 10; Length 1857;

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RESULT 141

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ADD03190 standard; cDNA; 1857 BP.

Novel human secreted and transmembrane protein PRO301 cDNA.
US2003104-A1.
15-WAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                          AUC90182 standard; CDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 CDNA.
US2003087348-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADD04594 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA
US2003087354-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA US2003092103-A1.
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Human secreted/transmembrane PRO polypeptide cDNA #27.
US2003105011-A1.
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                      PA (GETH.) GENENTECH INC.
Query Match
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 153
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(GETH ) GENENTECH INC.
ery Match 99.9%; Score 1840.4;
ery Match 99.9%; Pred. No. 0;
                                                                                      Score 1840.4;
Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
                                                                                                                                                                                                                                                                                 ADC69601 standard; cDNA; 1857 BP.
cDNA encoding human PRO polypeptide #183.
US2003194770-A1.
                                                                                                                                                                                                                                                                                                                                                                                                               Human PRO polynucleotide #183.
US2003194773-A1.
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Human PRO polynucleotide #183.
US2003194776-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADD11057 standard, cDNA, 1857 BP. Human PRO polynucleotide #183. US2003194774-A1.
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ID ADC47938 standard; CDNA; 1857 BP.
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08-MAY-2003.
(GFTH ) GENENTECH INC.
99.9%; SC
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08-MAY-2003.

(GETH ) GENENTECH INC.

99.9%;
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JS-JUN-2003.
(GETH ) GENENTECH INC.
99.9%; /
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16-007-2003.
(GETH ) GENENTECH INC.
99.9%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                  Best Local Similarity RESULT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
RESULT 154
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RESULT 155
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ADC48490 standard;
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(GETH) GENENTECH INC.
1:TY MATCh
1:T Local Similarity 99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 1857;
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                                                                                                      Length 1857;
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Novel human secreted and transmembrane protein cDNA Seg ID365.
US2003087363-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADCS3545 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein cDNA Seq ID355.
US2003087354-A1.
08-MAY-2003.
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Novel human secreted and transmembrane protein cDNA Seq ID365.
US2003087359-Al.
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Novel human secreted and transmembrane protein cDNA Seq ID365.
US2003087346-Al.
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Novel human secreted and transmembrane protein cDNA Seg ID365.
US2003087360-A1.
 AUC60484 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003087367-A1.
                                                                                                                                                      ADC50959 standard; cDNA; 1857 BP.

Wovel human secreted and transmembrane protein PRO301 cDNA. US2003087361-A1.
08-MAY-2003.
                                                              08-MAY-2003.
(GETH ) GENENTECH INC.
GETY MAtch 99.9%; Score 1840.4; DB 10;
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US2003082541-A1.
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(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
STY Match 99.9%; Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                 ADC65486 standard; cDNA; 1857 BP. Human PRO polynucleotide #183. US2003087362-A1. 08-MAY-2003.
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99.98;
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PA (GETH ) GENENTECH INC.
QUETY MATCh 99.9%;
BEST Local Similarity 99.9%;
RESULT 150
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                 Best Local Similarity
RESULT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                           Best Local Similarity RESULT 143
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RESULT 144
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RESULT 146

A D S E D

DB 10; Length 1857;

Length 1857;

DB 10;

Length 1857;

DB 10;

DB 10; Length 1857;

Length 1857;

DB 10;

Length 1857;

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US2003194792-A1.
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                                                                                                        99.9%; Score 1840.4; DB 10; Length 1857; 99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                              Length 1857;
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                                                                                                                                                                                                                                                                                                                                                                                                          ADC79998 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003087358-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADD11302 standard; cDNA; 1857 BP.
Human secreted/transmembrane PRO polypeptide cDNA #27.
US2003105013-A1.
(S5-UNA-2003.
(GETH ) GENENTECH INC.
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16-0CT-2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
ery Match
99.9%; Pred. No. 0;
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Human secreted/transmembrane protein cDNA, US2003104381-A1.
(G5-UTN-2003.
                                                                                                                                                                                                                                                                                                                              Score 1840.4;
Pred. No. 0;
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.9%; Score 1840.4; 99.9%; Pred. No. 0;
                                                                                                                                                                                       ADD04917 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA,
US2003104469-A1.
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Human secreted/transmembrane protein cDNA,
US2003108983-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding human PRO polypeptide #183.
US2003194769-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD09467 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003194775-A1.
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Human PRO polynucleotide #183.
US200319471.A1.
16-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
99.9%;
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Best Local Similarity 9
RESULT 165
ID ADD03499 standard; CDN
DE Human secreted/transme
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
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217 Match
Best Local Similarity
RESULT 163
ID ADD09467 stander
DE Human PRO r
PN US20031
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Best Local Similarity
RESULT 168
ID ADD53059 standard; Cl
DE CDNA encoding human
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Best Local Similarity
RESULT 164
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Best Local Similarity
                                                                                                                              Best Local Similarity RESULT 160
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30-OCT-2003.
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                                                                                                             Query Match
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30-OCT-2003.
(GETH ) GENENTECH INC.
ery Match 99.9%; Score 1840.4; DB 10; Length 1857;
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                             Length 1857;
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Novel human secreted and transmembrane protein PRO301 cDNA. US2003203432-A1.
                                                                           ADD53611 standard; cDNa; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003203437-A1.
                                                                                                                                                                                                                      #27
                             99.9%; Score 1840.4; DB 10; 99.9%; Pred. No. 0;
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Human secreted/transmembrane PRO polypeptide cDNA
US2003105012-A1.
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23-OCT-2003.
(GETH ) GENENTECH INC.
199.9%; Score 1840.4;
10ry Match 99.9%; Pred. No. 0;
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30-OCT-2003.
(GEH) GENENTECH INC.
10-TV Match 99.9%; Score 1840.4;
10-TV Match 99.9%; Pred. No. 0;
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Local Similarity 99.9%; Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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cDNA encoding human PRO polypeptide #183.
US2003194779-A1.
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Human PRO polynucleotide #183.
US2003199030-A1.
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Human PRO polynucleotide #183.
US2003199055-A1.
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Human PRO polynucleotide #183.
US2003199057-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADD02566 standard, cDNA, 1857 BP.
Human PRO polynucleotide #183.
US2003203431-A1.
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30-0CT-2003.
(GETH ) GENENTECH INC.
99.9%;
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30-0CT-2003.
(GETH ) GENENTECH INC.
99.9%;
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US2003203430-A1.
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16-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 172
                                                                                                                                                                     Best Local Similarity RESULT 170
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
RESULT 171
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Best Local Similarity
RESULT 174
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                                         Best Local Similarity RESULT 169
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Length 1857;

DB 10;

DB 10; Length 1857;

Length 1857;

DB 10;

DB 10; Length 1857;

DB 10; Length 1857;

Length 1857;

DB 10;

Length 1857;

DB 10;

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ADE32858 standard; cDNA; 1857 BP. Novel human secreted and transmembrane protein PRO301 cDNA.
                                                                                                                                                                                                                                                                                                                                                                  Human secreted/transmembrane protein cDNA, #25.
US2003077583-A1.
                     Ouery Match
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 187
                                                                                                                      PD 16-OCT-2003.

PA (GETH ) GENENTECH INC.

Query Match

Best Local Similarity 99.9%; Pred. No. 0;

RESULT 188
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PA (GETH ) GENENTECH INC.

Query Match

Best Local Similarity 99.9%; Pred. No. 0;

RESULT 190
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23-OCT-2003.
CGFH) GENENTECH INC.
199.9%; Score 1840.4;
1ery Match 99.9%; Pred. No. 0;
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Best Local Similarity 99.9%; Pred. No. 0;
RESULT 193
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Pred. No. 0;
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CDNA encoding human PRO polypeptide #183.
US2003199064-A1.
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ID ADD78908 standard; CDNA; 1857 BP. DE CDNA encoding human PRO polynemer PN US2003203429-A1.

PD 30-OCT-2001
                                                                            ADD93051 standard; cDNA; 1857 BP. Human PRO polynucleotide #183. US2003194768-A1.
                                                                                                                                                                                                                              ADE19471 standard; cDNA; 1857 BP. Human PRO polynucleotide #183. US2003199025-A1.
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US2003199059-A1.
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US2003199026-A1.
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US2003199033-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
     (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 191
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                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADE18919 standard;
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                                        Length 1857;
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003194767-A1.
                                                                                         ADE32306 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003194765-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003194791-A1.
                                        DB 10;
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16-OCT-2003.
(GETH) GENENTECH INC.
GETY MATCh 99.9%; SCOKE 1840.4;
Pred. No. 0;
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                                                                                                                                                                                                                                                               cDNA encoding human PRO polypeptide #183.
US2003199056-A1.
23-COT-2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4; pt Local Similarity 99.9%; Pred. No. 0;
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                                     Score 1840.4;
Pred. No. 0;
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                              ADD79462 standard; cDNA; 1857 BP.
cDNA encoding human PRO polypeptide #183.
US2003203428-A1.
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US2003207417-A1.
06-NOV-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE41998 standard; cDNA; 1857 BP. Human PRO polynucleotide #183. US2003194772-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADE17815 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003199023-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD91947 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003199053-A1.
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                                                                                                                                                                                                                                               ADE22238 standard; cDNA; 1857 BP
               Query Match 99.9%;
Best Local Similarity 99.9%;
RESULT 178
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(GETH ) GENENTECH INC.
                                                                                                                                                  16-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 182
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RESULT 180
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RESULT 181
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RESULT 184
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RESULT 186
23-OCT-2003
(GETH ) GEN
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Length 1857;

DB 10;

Length 1857;

DB 10;

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BERE
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E Human PRO polynucleotide #183.

N US2003207370-A1.

D 06-NOV-2003.

A (GETH ) GENENTECH INC.

Query Match

99.9%; Score 1840.4; DB 10; Length 1857;
     DB 10; Length 1857;
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207384-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADG21515 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207355-A1.
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  99.9%; Score 1840.4; 99.9%; Pred. No. 0;
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No. 0;
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PA (GETH) GENENTECH INC.
QUETY MATCh 99.9%; Score 1840.4;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 204
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Pred. No. 0;
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Pred. No. 0;
                                                                                                                                                      ADD80566 standard; cDNA; 1857 BP.
CDNA encoding human PRO polypeptide #183.
052003201418-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.9%; Score 99.9%; Pred.
                                          ADE42550 standard; cDNA; 1857 BP. Human PRO polynucleotide #183. US2003199032-A1.
                                                                                                                                                                                                                                                                     ADD89594 standard; cDNA; 1857 BP. Human PRO polynucleotide #183. US2001199028-Al. 23-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                 ADE40878 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003199031-A1.
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ID ADE92806 standard, cDNA, 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003194777-Al.
                       ... polynucleotide #1.
23-OCT-2003

PA (GETH) GENENTECH INC.
QUELY MATCh
Best Local Similarity 99.9%; SC
ID ADD80566 standard; CDN.
DE CDNA encoding hum.
PN US200320741°
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
Query Match
Best Local Similarity
RESULT 196
ID ADB42550 standard; cD
DE Human PRO polynucleot
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC
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Best Local Similarity
RESULT 200
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Best Local Similarity
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ID ADG231
DE Novel
PN US2003
PD 06-NOV
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DB 10; Length 1857;
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207381-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4; DB 10; Length st Local Similarity 99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADH55847 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207379-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA
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                                                                                                                                                                                                                                                                                                                                                   Human secreted/transmembrane polypeptide PR0301 cDNA. US2003170721-A1.
11-SEP-2003.
(GEXH) GENENTECH INC.
99.9%; Score 1840.4; DB 10; Let Local Similarity 99.9%; Pred. No. 0;
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US200303972-A1.
CFEB-2003.
(GETH ) GENENTECH INC.
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Human secreted/transmembrane protein cDNA, #25
US2003054352-A1.
                                                                                                                                      99.9%; Score 1840.4; 99.9%; Pred. No. 0;
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Best Local Similarity 99.9%; Pred. No. 0;
RESULT 212
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Best Local Similarity 99.9%; Pred. No. RESULT 205
                                                                                                                                                                                           CDNA; 1857 BP.
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                        ULT 205
ADG80555 standard; CDNA; 1857 B.
Human PRO polynucleotide #183.
US2003207373-A1.
06-NCV-2003.
(GETH ) GENENTECH INC.
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) GENENTECH INC.
99.9%; S.
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US2003207372-A1.
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PA (GETH ) GENENTECH INC.

Query Match 99.9%;

Best Local Similarity 99.9%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 206
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Best Local Similarity
RESULT 209
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Best Local Similarity
RESULT 211
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Best Local Similarity
                                                                                                                                                                                         ADG80003 standard;
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(GETH ) GEN
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ADM82545 standard; cDNA; 1857 BP.
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RESULT 2
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              AD163514 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207387-A1.
                                                                                                                                       ADH81928 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA, US2003200388-A1.
06-NOV-2003.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003032156-A1.
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Wovel human secreted and transmembrane protein PRO301 cDNA US2003207377-A1.
06-NOV-2003.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003040014-A1.
                                                                                            DB 10;
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                                                                                                                                                                                     06-NOV-2003.
(GETH ) GENENTECH INC.
2ry Match 99.9%; Score 1840.4;
2ry Match 99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                  06-NOV-2003.
(GETH ) GENENTECH INC.
199.9%; Score 1840.4;
STY Match 99.9%; Pred. No. 0;
                                                    OS-NOV-2003.
(GETH) GENENTECH INC.
(GETH) ABLCh 99.9%; Score 1840.4;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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cDNA encoding human PRO polypeptide #21
US2002192659-A1.
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Human PRO polynucleotide #21.
US2002146709-A1.
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20-MAR-2003.
(GETH ) GENENTECH INC.
99.9%;
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13-FBB-2003.
(GETH ) GENENTECH INC.
99.9%;
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(GETH ) GENENTECH INC.
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L.AY GENENTECH I.

LAY MATCH
BEST LOCAL SIMILATITY 9
RESULT 220
ID ACD42376 stand>
DE Novel humar
PN US2030**
PP 27-7
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
RESULT 218
                                                                                                      Best Local Similarity RESULT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 222
                                                                                                                                                                                                                                 Best Local Similarity
RESULT 216
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Best Local Similarity
RESULT 223
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RESULT 214
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Length 1857;
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Novel human secreted and transmembrane protein PRO301 cDNA. US2003087355-A1.
                                                                                                                  ADN15944 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA
US2003087353-A1.
                                                                                                                                                                                                                                                ADNI5573 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
                                                                                                                                                                                                                                                                                                                                                                  AUN15392 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA
US2003087356-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADN14840 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA
US2003087357-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC81102 standard, cDNA, 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA
US2003092115-A1.
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Pred. No. 0;
                                                                      DB 11;
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Human secreted/transmembrane protein cDNA, #25.
US2003135025-A1.
                                                                                                                                                                                                                                                                                           OB-MAY-2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
ery Match 99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
ry Match
t Local Similarity 99.9%; Pred. No. 0;
                                                                     Score 1840.4;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1840.4;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAY-2003.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
STY MATCh 99.9%; Pred. No. 0;
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No. 0;
                                                                                                                                                                                                  Score 1840.4;
Pred. No. 0;
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Pred.
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                                                                                                                                                      USZOUSU.
08-MAY-2003.
(GETH ) GENENTECH INC.
"MATCh "" " 109.9%;
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08-MXY-2003.
(GETH ) GENENTECH INC.
99.9%;
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15-MAY-2003.
(GETH ) GENENTECH INC.
99.9%;
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                                   PD 08-MAY-2003.

PA (GETH ) GENENTECH INC.

QUENY MATCh 99.9%;

BEST LOCAL Similarity 99.9%;
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                                            Best Local Similarity RESULT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                   US2003087385-A1.
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RESULT 243
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                                                            99.9%; Score 1840.4; DB 12; Length 1857; 99.9%; Pred. No. 0;
                                                                                                                                                                                      Length 1857;
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Human secreted/transmembrane PRO polypeptide cDNA #27.
US2003100497-A1.
                                                                                                                                                                                                                                                                                                                                                                                              USACOSTELE
10-JUL-2003.
(GETH ) GENENTECH INC.
(GETY MATCh
199.9%; Score 1840.4; DB 12;
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                                                                                                                                              US-cv---
10-JUL-2003.
(GETH ) GENENTECH INC.
(ELY Match 99.9%; Score 1840.4;
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29-MAY-2003.
(GETH) GENENTECH INC.
Hery Match 99.9%; Score 1840.4;
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15-MAY-2003.
(GETH) GENENTECH INC.
GETY MATCh 99.9%; Score 1840.4;
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15-MAY-2003.
(GETH ) GENENTECH INC.
HERY MATCh 99.9%; Score 1840.4;
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(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
ory Match 99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                           99.9%; Score 1840.4; 99.9%; Pred. No. 0;
                                                                                                         ADE79620 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA,
US2003130489-A1.
                                                                                                                                                                                                                                                                                                                                                                         Human secreted/transmembrane protein cDNA, US2003129592-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE23342 standard; cDNA; 1857 BP.
cDNA encoding human PRO polypeptide #183.
US2003092108-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE23894 standard; cDNA; 1857 BP.
cDNA encoding human PRO polypeptide #183.
US2003092110-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE24537 standard; cDNA; 1857 BP.
cDNA encoding human PRO polypeptide #183.
US2003092111-A1.
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.9%; Pred.
RESULT 232
ID ADE73296 standard; CDNA; 1857 BP.
DE Human secreted/transmembrane protein
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE89228 standard; cDNA; 1857 BP. Human PRO polynucleotide #183.
                                                                                                                                                                                                                              ADE75766 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003211571-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD87362 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003203439-A1.
Human PRO polynucleotide #183.
US2003203440-A1.
30-OCT-2003.
                                                                                                                                                                                                                                                                            13-NOV-2003.
(GETH ) GENENTECH INC.
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2003.
21 GENENTECH II.
2ry Match
Best Local Similarity 5
RESULT 240
ID ADD87362 standar'
DE Human PRO r'
PN US20032.
PD 30-
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2003.

21H ) GENENTECH I.

22Y MATCh

Best Local Similarity >
RESULT 239

ID ADE24537 stand>
DE cDNA encod*
PN US2030*
PD 15-**
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(GETH ) GENENTECH INC.
                                              GENENTECH INC.
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RESULT 241
ID ADE89228
                                                                                                                                                                              Query Match In
Best Local Similarity
RESULT 234
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Best Local Similarity
RESULT 238
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Best Local Similarity
RESULT 237
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RESULT 236
                                                           Query Match
Best Local Similarity
RESULT 233
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   PN PN
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23-OCT-2003.
(GETH) GENENTECH INC.
ery Match 99.9%; Score 1840.4; DB 12; Length 1857;
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(GETH) GENENTECH INC.
ery Match
29.9%; Score 1840.4; DB 12; Length 1857;
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                                  Length 1857;
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                                                                                    ADE41185 standard; cDNA; 1857 BP.
Human secreted/transmembrane polypeptide PRO301 cDNA.
US2003104558-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12;
                                  DB 12;
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                                                                                                                                                                                                                                                                                                                      DB 12;
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US2003211576-A1.
                                                                                                                                                                                                                                                  #25
                                  99.9%; Score 1840.4; 99.9%; Pred. No. 0;
                                                                                                                                  GETH) GENENTECH INC.

(GETH) GENENTECH INC.

199.9%; Score 1840.4;

1ery Match

29.9%; Pred. No. 0;
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07-AUG-2003.

(GETH ) GENENTECH INC.

99.9%; Score 1840.4;

erv Match

99.9%; Pred. No. 0;
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PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity , 99.9%; Pred. No. 0;
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Human PRO polynucleotide #183.

US2003199061-A1.

23-OCT-2003.

(GETH) GENENTECH INC.

99.9%; Score 1840.4;

st Local Similarity 99.9%; Pred. No. 0;
                                                                                                                                                                                                                              ADE73831 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA,
US2003148370-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE94696 standard; cDNA; 1857 BP.
cDNA encoding human PRO polypeptide #183.
US2003199027-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 249
ID ADE95248 standard; CDNA; 1857 BP.
DE CDNA encoding human PRO polypeptide #183.
PN US2003199052-A1.
                                                                                                                                                                                                                                                                                                                                                                      ADE18367 standard; cDNA; 1857 BP. Human PRO polynucleotide #183. US2003194794-A1. 16-OCT-2003. (GETH ) GENENTECH INC.
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Human PRO polynucleotide #183.
US2003199060-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA; 1857 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA; 1857 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human PRO polynucleotide #183.
US2003199054-A1.
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(GETH ) GENENTECH INC.
23-OCT-2003.
(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 248
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RESULT 250
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                                             Best Local Similarity RESULT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 245
ID ADE88676 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE99385 standard;
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Best Local S
                                      Query Match
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Length 1857;
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Query Match 99.9%; Score 1840.4; DB 12; Length 1857;
                                                                                                                                                                                                                                                                                                                                                                                                             ADE92254 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003199051-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE91702 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003199058-A1.
                                                                                                                                                                                                          99.9%; Score 1840.4; DB 12; 99.9%; Pred. No. 0;
                                                           DB 12;
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                                                                                                                                                                                                                                                            ADE98504 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA, #25.
US2003211569-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADE98931 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA, #25.
US2003211568-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted/transmembrane protein cDNA, #25.
US2003225253-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADF73795 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA, #25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-NOV-2003.
(GETH ) GENENTECH INC.
P9.9%; Score 1840.4;
FY Match 99.9%; Pred. No. 0;
                                                         Score 1840.4;
Pred. No. 0;
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Pred. No. 0;
                                                                                                            ADF34939 standard; cDNA; 1857 BP.
CDNA encoding human PRO polypeptide #183.
23.0CT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADE90555 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003199063-A1.
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                                                                                                                                                                                                                                                                                               US2003411.
13-NOV-2003.
(GETH ) GENENTECH INC.
99.9%; SC
23-OCT-2003.
(GETH ) GENENTECH INC.
99.9%;
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23-007-2003.
(GETH ) GENENTECH INC.
99.9%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                   Best Local Similarity
RESULT 251
ID ADF34939 standard; CD
DE CDNA encoding human P
PN US2003199029-A1.
PD 23-0CT-2003.
PA (GETH ) GENENTECH INC
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Best Local Similarity
RESULT 253
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Best Local Similarity
RESULT 254
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Best Local Similarity
RESULT 257
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25-SEP-2003.
                                                         Query Match
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Length 1857;.
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ry Match
+ Tocal Similarity 99.9%; Pred. No. 0;
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Novel human secreted and transmembrane protein PRO301 CDNA.
US2003207360-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003207426-Al.
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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JG-NOV-2003.
(GETH ) GENENTECH INC.
99.9%; SCORE LDT...
99.9%; Pred. No. 0;
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US2003207376-A1.
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cDNA encoding human PRO polypeptide #183.
US2003207359-A1.
Best Local Similarity 99.9%; Pred. No. RESULT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADF98043 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003207422-A1.
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                                 ADG02281 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003207352-A1.
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Human PRO polynucleotide #183.
US2003207353-A1.
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06-NOV-2003.
(GETH ) GENENTECH INC.
99.9%; Sr
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06-NOV-2003.
(GETH ) GENENTECH INC.
99.9%;
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h 99.9%;
Similarity 99.9%;
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(GETH ) GENENTECH INC.
2ry Match 99.9%;
3t Local Similarity 99.9%;
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(GETH ) GENENTECH INC.
                                                                                                                                 Best Local Similarity RESULT 260
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Best Local Similarity
RESULT 266
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DB 12; Length 1857;
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Novel human secreted and transmembrane protein PRO301 cDNA,
US2003207424-Al.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003207389-A1.
                                                                                                                                                                                                          99.9%; Score 1840.4; DB 12; 99.9%; Pred. No. 0;
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OG-NOV-2003.

(GETH) GENENTECH INC.

99.9%; Score 1840.4;

Pred. No. 0;
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04-SEP-2003.
(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
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Pred. No. 0;
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                                                                                                                                                CDNA encoding human PRO polypeptide #183.02003207425-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                  ADG13314 standard; cDNA; 1857 BP.
CDNA encoding human PRO polypeptide #183.
US2003207357-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADGIS541 standard; cDNA; 1857 BP.
CDNA encoding human PRO polypeptide #183.
22003219885-A1.
27-NOV-2003.
                   BP.
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Human PRO polynucleotide #183.
US2003207371-A1.
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Human PRO polynucleotide #183.
US2003207374-A1.
                                                                                                                                   ADG19477 standard; cDNA; 1857 BP
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          Human PRO polynucleotide #183. US2003207375-A1.
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(GETH ) GENENTECH INC.
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2003.
2003.
2ry Match
Best Local Similarity 5
RESULT 273
ID ADG15541 stand*
DE cDNA encod*
PN US2037*
PD 27-
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 272
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Best Local Similarity
RESULT 271
RESULT 268
ID ADG05210 standard;
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Best Local Similarity
RESULT 275
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Best Local Similarity
RESULT 277
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Length 1857;
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Query Match
Best Local Similarity 99.9%; ....
Best Local Similarity 99.9%; ....
RESULT 283
ID ADG62010 standard; cDNA; 1857 BP.
DE ADG62010 standard; cDNA; 1857 BP.
DE NOVech human secreted and transmembrane protein PRO301 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
PA (GETH) GENENTECH INC.
Ouery Match
Ouery Match
' cimilarity 99.9%; Pred. No. 0;
                                                                                                                                 ADG24898 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207427-Al.
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Novel human secreted and transmembrane protein PRO301 cDNA
US2003194778-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA.
                                                                                                                                                                                                                                                                     ADG07195 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PR0301 US2003207350-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                    Score 1840.4; DB 12;
Pred. No. 0;
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(GETH) GENENTECH INC.

99.9%; Score 1840.4;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
ADG03997 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003207423-A1.
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Human PRO polynucleotide #183.
US2003207358-A1.
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36-NOV-2003.
(GETH ) GENENTECH INC.
99.9%; /
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06-NOV-2003.
(GETH ) GENENTECH INC.
99.9%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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06-NOV-2003.
(GETH ) GENENTECH INC.
99.9%;
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(GETH ) GENENTECH INC.
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RESULT 285
ID ADG82211 standard; cl
DE Human PRO polynucleof
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC
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Best Local Similarity
RESULT 279
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Best Local Similarity
RESULT 282
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Best Local Similarity
RESULT 286
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US2003207805-A1.
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                                                                                                                                                                                                                                                                                     RESULT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
                                                         Length 1857;
                                                                                                                                                                                                                                                                                                                                                                                                       99.9%; Score 1840.4; DB 12; Length 1857; 99.9%; Pred. No. 0;
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207363-A1.
Novel human secreted and transmembrane protein PRO301 cDNA.
                                                                                                          Novel human secreted and transmembrane protein PRO301 cDNA US2003207364-A1.
                                                                                                                                                                                                      ADG55794 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA
US2003207365-A1.
                                                                                                                                                                                                                                                                                                                              ADGS6554 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                ADG70920 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA
US2003207420-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADG53586 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA
US2003207415-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADG71472 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 CDNA
US2003207421-A1.
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Pred. No. 0;
                                                                                                                                                                        DB 12;
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                                                       DB 12;
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US2003027146-Al.
06-FEB-2003.
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A. 99.9%; Score 1840.4;

A. 99.9%; Pred. No. 0;
                                                                                                                                                                      Score 1840.4;
Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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                                                       Score 1840.4;
Pred. No. 0;
                                                                                                                                                                                                                                                                                     Score 1840.4;
Pred. No. 0;
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                                                                                                 ADG56898 standard; cDNA; 1857 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADG92641 standard; cDNA; 1857 BP
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06-NOV-2003.
(GETH ) GENENTECH INC.
99.9%; S'
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06-NOV-2003.
(GETH ) GENENTECH INC.
99.9%;
             (GETH ) GENENTECH INC.
99.9%;
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06-NOV-2003.
(GETH ) GENENTECH INC.
99.9%;
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06-NOV-2003.
(GETH ) GENENTECH INC.
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                                                                                                                                                                     Query Match
Best Local Similarity
RESULT 288
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Best Local Similarity
RESULT 290
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RESULT 293
                                                                Best Local Similarity RESULT 287
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          US2003207362-A1.
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(GETH ) GEN
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ID ADG816
DE Human
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06-NOV-2003.
(GETH) GENENTECH INC.
ery Match 99.9%; Score 1840.4; DB 12; Length 1857;
            Length 1857;
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                                                                                                                                                                                                                                                                                                                                                  Novel human secreted and transmembrane protein PRO301 cDNA US2003207419-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUG52410 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207414-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADG54138 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207416-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADH11612 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA
US2003207378-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADG61458 standard, cDNA, 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA
US2003207429-A1.
                                                                                                                                                                                                              Human secreted/transmembrane polypeptide PRO301 cDNA.
US2003180796-A1.
25-SEP-2003.
            DB 12;
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Pred. No. 0;
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(GETH ) GENENTECH INC.
99.9%; Score 1840.4;
EXY Match 99.9%; Pred. No. 0;
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16-OCT-2003.
(GETH ) GENENTECH INC.
ery Match 99.9%; Score 1840.4;
                                                                                                                                              99.9%; Score 1840.4; 99.9%; Pred. No. 0;
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Pred. No. 0;
            99.9%; Score 1840.4; 99.9%; Pred. No. 0;
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Pred. No. 0;
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Pred. No. 0;
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US2003194793-A1.
                                                           ADH30621 standard; cDNA; 1857 BP. Human PRO polynucleotide #183. US2003077723-A1.
                                                                                                                                                                                                   CDNA; 1857 BP
                                                                                                                                                                                                                                                                                                                                      ADH11988 standard; cDNA; 1857 BP
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25-SEP-2003.
(GETH ) GENENTECH INC.
99.9%; Sr
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                                                                                                             24-APR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                                           Best Local Similarity RESULT 297
              Query Match
Best Local Similarity
RESULT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                   ADG63620 standard;
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06-NOV-2003.
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Query Match
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ID ADI153
DE Novel
PN US2003
PD 06-NOV
                                                                                           RESULT 313
                                                                                                                                    DB 12; Length 1857;
                                                                                                                                                                                                                                                                                                                                                 99.9%; Score 1840.4; DB 12; Length 1857; 99.9%; Pred. No. 0;
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                             Length 1857;
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                                                                                                                                                                                                                                                                                ADG59730 standard; cDNA; 1857 BP.

Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207369-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                      ADG54690 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA
US2003207367-A1.
06-NOV-2003.
                             DB 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted/transmembrane protein cDNA, #25.
US2004006211-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 305
                                                              ADH28545 standard; cDNA; 1857 BP.

Human PRO polynucleotide #183.

30-JAN-2003.

(GETH ) GENENTECH INC.

99.9%; Score 1840.4;

st Local Similarity 99.9%; Pred. No. 0;
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(GETH ) GENENTECH INC.
2ry Match 99.9%; Score 1840.4;
2ry Match 99.9%; Pred. No. 0;
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08-2NA-2004.
(GETH) GENENTECH INC.
99.9%; Score 1840.4;
ery Match
99.9%; Pred. No. 0;
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Pred. No. 0;
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Human secreted/transmembrane protein cDNA,
US2004005553-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted/transmembrane protein cDNA, US2003215904-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADH43486 standard; cDNA; 1857 BP.
Human PRO polynucleotide #27.
US2003224984-A1.
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ID ADH59830 standard; cDNA; 1857 BP
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JAN-2003.
(GETH) GENENTECH IN
Query Match
Best Local Similarity 91.
RESULT 306
ID ADG54690 standar
PE Novel human
PD US20032"
PD 06-20032"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DESN/) DESNOYERS L.
(GODD/) GODDWARD A.
(GURN/) GURNEY A L.
(MATH/) MATHER J P.
(WILL/) WILLIAMS P M.
(WOOD/) WOOD W I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-DEC-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-JAN-2004.
(DESN/) DESNOYERS L.
(GODD/) GODDARD A.
(GODO/) GODOWSKI P J.
                                                                                                                                                                                                                                                    Best Local Similarity RESULT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
RESULT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Length 1857;
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207382-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADG09245 standard; cDNA; 1857 BP. Novel human secreted and transmembrane protein PRO301 cDNA. US2004009547-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human secreted and transmembrane protein PRO301 cDNA US2004009548-A1.
                                                                        DB 12;
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(GETH ) GENENTECH INC.

199.9%; Score 1840.4; DB 12;

Lery Match

99.9%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted/transmembrane protein cDNA, #25.
US2003096340-A1.
22-MAY-2003.
(GETH) GENENTECH INC.
ery Match
St Local Similarity 99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                          ADI18600 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA, #25.
US2003152999-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADI65747 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA, #25.
                                                                                                                                                                                                                                                                                                                                                                                                                                               #25
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                                                                        99.9%; Score 1840.4; 99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                        USACCOLOR 14-AUG-2003.
(GETH ) GENENTECH INC.
199.9%; Score 1840.4;
Hery Match 99.9%; Pred. No. 0;
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PA (GETH ) GENENTECH INC.

Query Match 99.9%; Score 1840.4;

Best Local Similarity 99.9%; Pred. No. 0;

RESULT 318
                                                                                                                                                                                                                      Score 1840.4;
Pred. No. 0;
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 315

ID AD165320 standard; cDNA; 1857 BP.

DE Human secreted/transmembrane protein cDNA, PN US2003148419-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADH97379 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA, US2003190610-A1.
(GETH ) GENENTECH INC.
                                                                                                                                             cDNA encoding human PRO polypeptide #183.
US2003207361-A1.
                                                                                                                              ADI81154 standard; cDNA; 1857 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA; 1857 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADG09897 standard; cDNA; 1857 BP
                                                                                                                                                                 S2003zv.
J6-NOV-2003.
(GFTH) GENENTECH INC.
99.9%;
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15-07N-2004.
(GETH ) GENENTECH INC.
99.9%;
(GURN/) GURNEY A L.
(MATH/) MATHER J P.
(WILL/) WILLIAMS P M.
(WOOD/) WOOD W I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-AUG-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
RESULT 320
                                                                                                                                                                                                                                      Best Local Similarity RESULT 314
                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 317
                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADI37583 standard;
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us-10-785-220b-11.rng.spdi

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99.9%; Score 1840.4; 99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                            99.9%; Score 1840.4; 99.9%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                           ADJ65593 standard; cDNA; 1857 BP.
cDNA encoding human PRO polypeptide #183.
US2004038335-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA encoding human PRO polypeptide #183
US2004048333-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding human PRO polypeptide #183 US2004058424-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADM28315 standard; cDNA; 1857 BP.
cDNA encoding human PRO polypeptide #183.
US2004077064-A1.
                                                                                                                                                                                    ADK82831 standard; cDNA; 1857 BP.
Human PRO polynucleotide #27.
US2004043927-A1.
                                               ADJ77471 standard; cDNA; 1857 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA; 1857 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADR17914 standard; cDNA; 1857 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA; 1857 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADM42453 standard; cDNA; 1857 BP
                                                                   Human PRO polynucleotide #183. US2004038336-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human PRO polynucleotide #23
US6686451-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                              26-FEB-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GERRITSEN M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOTSTEIN D.
DESNOYERS L.
EATON D L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASHKENAZI A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FERRARA N.
FILVAROFF E.
            Best Local Similarity RESULT 330
                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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RESULT 335
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Best Local Similarity
RESULT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADM27729 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADO06153 standard;
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                                                                                                                                                                                                                                                                           Query Match
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 Query Match
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(GERR/)
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          07-AUG-2003.
(GETH ) GENENTECH INC.
ery Match 99.9%; Score 1840.4; DB 12; Length 1857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.9%; Score 1840.4; DB 12; Length 1857; 99.9%; Pred. No. 0;
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                                                                                   ADI14700 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADI18295 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207349-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ63576 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA. US2004039164-A1.
26-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GG-NOV-2003.
(GETH ) GENENTECH INC.
(ery Match 99.9%; Score 1840.4; DB 12;
ery Match 99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12;
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Human secreted/transmembrane protein cDNA, #25.
US2003186358-A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                    ADH60490 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA, #25.
US2004023331-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADM25081 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA, #25.
US2003096233-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADM29831 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA, #25.
US2003190611-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ99547 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA, #25.
US2003187238-A1.
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(GETH ) GENENTECH INC.
12 Match 99.9%; Score 1840.4;
21 Match 99.9%; Pred. No. 0;
                                                                                                                                          US.c.-..
06-NOV-2003.
(GETH ) GENENTECH INC.
ery Match 99.9%; Score 1840.4;
                                                                                                                                                                                                                                                                                                                                                                                                                               99.9%; Score 1840.4; 99.9%; Pred. No. 0;
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Pred. No. 0;
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02-OCT-2003.
(GETH ) GENENTECH INC.
99.9%;
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.8738-A1.
.CT-2003.
(GETH ) GENENTECH 1.
Query Match
Best Local Similarity P.
RESULT 326
ID ADL08740 stand DE Human secreting PN US20031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                         DESNOYERS L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
RESULT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity
RESULT 325
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 323
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                                                          Best Local Similarity
RESULT 322
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US2003148371-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best RESULT
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22-APR-2004.
(GETH ) GENENTECH INC.
ery Match 99.9%; Score 1840.4; DB 12; Length 1857;
Length 1857;
                                                                                                Length 1857;
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DB 12;
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                                                                                                DB 12;
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                                                                                                                                                                                                                                                                                                                                                                                                      DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted/transmembrane protein cDNA, #25
                                                                  GETH) GENENTECH INC.

(GETH) GENENTECH INC.

199.9%; Score 1840.4;

197.04;

198.9%; Pred. No. 0;
                                                                                                                                                                 USZUCZ-...
04-MAR-2004.
(GETH) GENENTECH INC.
18rv Match 99.9%; Score 1840.4;
                                                                                                                                                                                                                                                                                                                                                                     PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Bost Local Similarity 99.9%; Pred. No. 0;
RESULT 334
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(TUMA/) TUMAS D.
(WILL/) WILLIAMS P M.
(WOOD/) WOOD W I.
STEWART I A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WOOD W I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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(STEW/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NAPI/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J;

Jin CDNA, #25.

JNA; 1857 BP.

JOAGUELON O;

JOAGUELON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PD 14-AUG-2003
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 99.9%; Score 1840.4; DB 13; Length 1857;
RESULT 341
ID ADT94259 standard; CDNA, 1857 BP.
DE Human PRO301 cDNA sequence.
PN AU2003259607-A1.
PD 27-NOV-2003
PA (GETH) CONTRIBET CONTRIBET BP.
PN AU2003259607-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 99.9%; Score 1840.4; DB 13; Length 1857;
Best Local Similarity 99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                      99.9%; Score 1840.4; DB 13; Length 1857; 99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13; Length 1857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADI96349 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207354-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.9%; Score 1840.4; 99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                     ADI95797 standard; cDNA; 1857 BP.
cDNA encoding human PRO polypeptide #183.
US2003077659-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-APR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                      (PANJ) PAN J.
(PANJ) PAN J.
(ROYM) ROY M A.
(STEW) STEWART T A.
(TUNA) TUNAS D.
(WILL) WILLIAMS P M.
(WOOD)) WOOD W I.
                     GODOWSKI P J.
GRIMALDI C J.
                                                                                                           KLJAVIN I J.
MATHER J P.
                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity
RESULT 339
                                                                GURNEY A L.
HILLAN K J.
GODDARD A.
                                                                                                                                                                                                                                                                                                                      Ouery Match
                                                                                      (HILL/)
(KLJA/)
(MATH/)
                   GODO/)
                                                                  GURN/)
PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BARA
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99.9%; Score 1840.4; DB 13; Length 1857; 99.9%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                 DB 4; Length 1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5; Length 3389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5; Length 3389;
                                                                                                                                                                DB 4; Length 2259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE08895 standard; DNA; 1902 BP.
Novel DNA-related contig nucleotide sequence #139.
WO2003054152-A2.
                                                                                                                                                                                                                                                                                                                                                                                       AAS22710 standard, cDNA, 1902 BP.
Human cDNA encoding a novel human protein #276.
WO200155437-A2.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                Human cDNA encoding a novel human protein #275.
WO200155437-A2.
                                                                               3 Human cDNA encoding a novel human protein #39.
N W0200155437-A2.
O 22-AUG-2001.
A HYSEJ HYSEQ INC.
99.6%; Score 1834; DB 4
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human prostate expression marker cDNA 28094.
WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PD 33-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 99.3%; Score 1829.2;
Best Local Similarity 99.6%; Pred. No. 0;
RESULT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABV22266 standard; cDNA; 3389 BP.
Human prostate expression marker cDNA 22257.
WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human DNA40628 cDNA encoding PRO301 protein.
US2003171568-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.2%; Score 1827.6; 99.5%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.3%; Score 1829.2; 99.6%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.3%; Score 1829.2; 99.6%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 99.3%; Score 1829.2;
Local Similarity 99.6%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                             99.3%; Score 1829.2; 99.6%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-AUG-2001.
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                 uery Match
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 344
                                                                                                                                                                                                                          AAS22709 standard; cDNA; 1902 BP.
                                                              CDNA; 2259 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABV28103 standard; cDNA; 3389 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 99.5%; Preference To Anna S294 standard, DNA, 1842 BP.

DE Human PRO301 gene DNA40628.

PN W02004031105-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADH62538 standard; cDNA; 1842 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-SEP-2003.
(ASHK/) ASHKENAZI A.
(FONG/) FONG S.
(GODD/) GODDARD A.
(GURN/) GURNEY A L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
RESULT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FONG S.
GODDARD A.
GURNEY A L.
NAPIER M A.
TUMAS D.
               Best Local Similarity RESULT 343
                                                            AAS22473 standard;
                                                                                                                                                                                                                                                                                      02-AUG-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUL-2003.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-APR-2004
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AAD08335 standard; cDNA; 1918 BP.
Human secreted protein-encoding gene 23 cDNA clone HACAA29, SEQ ID NO:63.
WO200136440-A1.
                            DB 13; Length 3861;
                                                                                                                                                                                                                                                                                                                                               DB 12; Length 1822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13; Length 1822;
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                                                                                                                                                                                    Length 1918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADR41346 standard; cDNA; 1897 BP.
Human CD-like molecule HKACI03 cDNA, SEQ ID NO:145.
                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS28784 standard; cDNA; 1812 BP.
Human immunoglobulin encoding cDNA SEQ ID No 30.
WO200155315-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                           ADK40842 standard; cDNA; 1822 BP.
DNA encoding human platelet F11 receptor #1.
US6699688-B1.
                                                                                                                                                                                                                                                                                                                                           97.5%; Score 1796.4; 99.7%; Pred. No. 0;
                          Score 1812.8;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1793.2;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1788.4;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.4%; Score 1682.8; 95.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
ry Match
L Local Similarity 95.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1682.8;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cDNA encoding a novel protein SEQ ID US2003077606-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN GENOME SCI INC.
1
1 Similarity 95.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADR27640 standard; cDNA; 1822 BP.
Full length human F11 receptor cDNA Seq 6.
WO2004063327-A2.
                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.

(HUMA-) HUMAN GENOME SCI INC.

97.7%; Score 1800;

ery Match

97.7%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                         (UYNY ) UNIV NEW YORK STATE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABV83791 standard; cDNA; 1812 BP.
Human polynucleotide SEQ ID NO 120.
US2002090672-A1.
                                                                                                                                                                                                                                                                                                                                                                                                   ADN05139 standard; cDNA; 2187 BP. Antipsoriatic cDNA sequence #785. WO2004028479-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABA06454 standard; cDNA; 1812 BP.
Human cDNA SEQ ID NO: 120.
WO200154474-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB31509 standard; cDNA; 1812 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                            28477
-2004.
) GENENTECH INC.
97.4%; Sr
99.2%; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
                          98.4%;
99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BABI/) BABINSKA A. (EHRL/) EHRLICH Y H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                           Best Local Similarity
RESULT 360
                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
RESULT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (RUBE/) RUBEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KORN/) KORNECKI E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-APR-2004
                                                                                                                                                                                                                                                                                                      02-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-APR-2003
(HUMA-) HUN
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 367
                                                                                                                                                                                                                                                                                                                                                                                                   AAD08305 standard; cDNA; 1915 BP.
Human secreted protein-encoding gene 23 cDNA clone HACAA29, SEQ ID NO:33.
WQ200116440-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUK46576 standard; DNA; 3861 BP.
Human Fll receptor (FllR) transcript variant 4, encoding gene, SEQ ID 7.
02-SEP-2004.
                                                                                                                                                                                                                                                   ADR46578 standard; DNA; 3794 BP.
Human JAM-1, F11 receptor (F11R) transcript variant 5, encoding gene.
JP20044242513-A.
02-SEP-2004.
(DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
99.0%; Score 1824.4; DB 13; Length 3794;
st Local Similarity 99.4%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADR46570 standard; DNA; 3660 BP.
Human JAM-1, F11 receptor (F11R) transcript variant 1, encoding gene.
JP2004242513-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.5%; Score 1814.8; DB 13; Length 2141; 99.1%; Pred. No. 0;
                                           DB 12; Length 1842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
ry Match 99.0%; Score 1822.8; DB 13; Length 3660;
t Local Similarity 99.3%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12; Length 2100;
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                                                                                                                                                                                                    Length 1831;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant vector preparation human clone cDNA, PLACE1005544. JP2004215665-A.
                                                                                                ABX93343 standard; cDNA; 1831 BP.
cDNA DNA40628 encoding human A-33 related antigen PRO301.
US2002182206-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12;
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8
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                                                                                                                                                                                                    DB
(GETH ) GENENTECH INC.

99.2%; Score 1827.6;

Match 99.5%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WOLVELL
25-MAY-2001.
(HUMA-) HUMAN GENOME SCI INC.
(ery Match 99.0%; Score 1822.8;
ery Match 99.3%; Pred. No. 0;
                                                                                                                                                       PD 05-DEC-2002.

PA (GETH) GENENTECH INC.

Query Match 99.1%; Score 1826.2;

Best Local Similarity 99.8%; Pred. No. 0;

RESULT 352
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ery Match

98.7%; Score 1817.6;
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(HELL-) HELIX RES INST.
(HELL-) HELIX RES INST.
98.5%; Score 1814.8;
ery Match
'amilarity 99.1%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.5%; Score 1814.8; 99.1%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAK94509 standard; cDNA; 2141 BP.
Human full-length cDNA, SEQ ID NO: 3364.
EP1130094-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADL31331 standard; cDNA; 2141 BP.
Full length human cDNA clone SeqID 3364.
EP1396543-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADL26799 standard; cDNA; 2100 BP.
Human JAM1 encoding cDNA SEQ ID NO:53.
WO2004022778-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADQ68025 standard; cDNA; 2141 BP.
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                    PA (GETH ) GENENTECH 11
Query Match
Best Local Similarity
RESULT 351
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RESULT 357
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Best Local Similarity
RESULT 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity RESULT 359
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                                                                                                                                                                                                                                                                                                                                                            Query Match
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Query

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Best

RESULT ID AAD DE HU PN. WC PD 25

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Best_Local Similarity
RESULT 379
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Best Local Similarity
RESULT 384
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                                                                                                                                                                                                                                                                                                                                                                                            ADE07127 standard; DNA; 1943 BP.

Novel coding sequence (useful for identifying genetic disorders) #193.

WO2003054152-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADR46572 standard; DNA; 2009 BP.
Human JAM-1, F11 receptor (F11R) transcript variant 4, encoding gene.
JP2004242513-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADR46574 standard; DNA; 3527 BP.
Human JAM-1, F11 receptor (F11R) transcript variant 3, encoding gene.
JP2004242513-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-SEP-2004.
(DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
ery Match 84.8%; Score 1562.8; DB 13; Length 3527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match
Best Local Similarity 99.8%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                             Length 4249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1943;
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                                                                                  DB 7; Length 1897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 2066;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1772
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cDNA encoding human A33 receptor homologue, SEQ ID NO:70.
W09955865-A1.
                                                                                                                                                                                                                                                                                                                DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL34760 standard; cDNA; 1421 BP.
Human cDNA isolated from skin cells SEQ ID NO: 70.
WO200190357-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX37716 standard; DNA; 2066 BP.
Human cDNA clone DNA35936 consensus sequence.
WO9914241-A2.
                                                                                  91.0%; Score 1675.4; 95.8%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.4%; Score 1351.2; 99.3%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.9%; Score 1637.4; 99.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.7%; Score 1614.6;
99.1%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GY-NOV-2001.

(HUMA-) HUMAN GENOME SCI INC.

(RTMA-) HUMAN GENOME SCI INC.

(RTM MAtch

(R
                                                                                                                                                                                                                                                                                                             90.3%; Score 1663.8; 91.8%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.4%; Score 1351.2; 99.3%; Pred. No. 0;
                                                                                                                                                                  ADJ67405 standard; DNA; 4249 BP.
Human ovarian specific gene SEQ ID NO:119.
WO2004013311-A2.
12-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL90699 standard; cDNA; 1772 BP.
Human polynucleotide SEQ ID NO 1261.
WO200190304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENE-) GENESIS RES & DEV CORP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-NOV-2000.
(GENE-) GENESIS RES & DEV CORP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC99608 standard; cDNA; 1421 BP.
Skin cell cDNA, SEQ ID NO: 70.
WO200069884-A2.
                          04-APR-2002.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A2.
-1999.
-24Ty Match
Best Local Similarity 5
RESULT 373
ID ABL90699 stand*
DE Human polv*
PN WO2001**
PA
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                     (DIAD-) DIADEXUS INC.
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Best Local Similarity
RESULT 374
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Best Local Similarity
RESULT 375
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Best Local Similarity
RESULT 371
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Best Local Similarity
RESULT 376
                                                                                                    Best Local Similarity RESULT 369
                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUL-2003.
(HYSE-) HYSEO INC.
WO200226930-A2.
                                                                                                                                                                                                                                                                                                             Query Match
                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BERE
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DB 12; Length 4633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 1421;
                                                                                                            Length 1421;
                                                                                                                                                                                                                                                                                           DB 3; Length 1421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6; Length 1421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12; Length 1236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAL51598 standard; DNA; 900 BP.
Human junctional adhesion molecule 1 (huJAM1) coding sequence
WO2003008541-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV28136 standard; cDNA to mRNA; 924 BP.
Human junctional adhesion molecule gene.
MO9824897-A1.
11-JUN-1998.
(HOFF) HOFFMANN LA ROCHE & CO AG F.
2TY Match 42.8%; Score 787.6; DB 2; Length 924; St Local Similarity 95.1%; Pred. No. 2.5e-242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2003.
1 (ELIL ) LILLY & CO ELI.
Query Match 48.9%; Score 900; DB 8; Length 900;
Best Local Similarity 100.0%; Pred. No. 1.5e-278;
                                                                                                                                                                            AAZ61781 standard; cDNA; 1421 BP.
cDNA encoding human A33 receptor homologue, SEQ ID NO:254.
WO9955865-A1.
                                                                                                              DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
vuery Match

vuery Match

Best LTD.

73.4%; Score 1351.2; DB

Best Joe

RESULT 308

ID AAZ61781 standard; CDVA; 1421 BP

DE CDNA encoding human A33

PD 04-NOV-100

PA NOV-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL34866 standard; cDNA; 1421 BP.
Human cDNA isolated from skin cells SEQ ID NO:
WO200190357-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1279.8;
Pred. No. 0;
                                                                                                                                                                                                                                                                                           73.3%; Score 1350.4; 99.6%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.3%; Score 1350.4; 99.6%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENE-) GENESIS RES & DEV CORP LTD.

(GENE-) GENESIS RES & DEV CORP LTD.

73.3%; Score 1350.4;

""" cimilarity 99.6%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.8%; Score 1047; 1100.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.8%; Score 1028; 100.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADJ67404 standard; DNA; 4633 BP.
Human ovarian specific gene SEQ ID NO:118.
02004013311-A2.
(DIAD-) DIADEXUS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AD095889 standard; cDNA; 1236 BP.
T cell activation associated cDNA #34.
W02004058805-A2.
15-JUL-2004.
(ASAH-) ASAHI KASEI PHARMA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADQ95891 standard; cDNA; 1116 BP.
T cell activation associated cDNA #35.
WO2004058805-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENE-) GENESIS RES & DEV CORP LTD
                                                                                                                                                                                                                                                                                                                                                         AAC99714 standard; cDNA; 1421 BP.
Skin cell cDNA, SEQ ID NO: 254.
WO200069884-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX21837 standard; cDNA; 1140 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JAN-1999.
(SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F11 antigen coding sequence.
W09902561-A1.
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03-JUN-1999.
(GETH ) GENE
                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                       (ASHK/)
(FONG/)
(GODD/)
(GURN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                            (NAPI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB53509 standard; DNA; 1895 BP.
Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4051.
WO2003065993-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-Aug-zous.
(GENE-) GENE LOGIC INC.
ry Match
rocal Similarity 75.5%; Pred. No. 2.1e-203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 35.0%; Score 644.6; DB 13; Length 2453;
Best Local Similarity 73.7%; Pred. No. 5.4e-196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-4UG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ery Match
39.5%; Score 727.2; DB 4; Length 1894;
ery Match
71.6%; Pred. No. 1.1e-222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.5%; Score 727.2; DB 6; Length 1894; 71.6%; Pred. No. 1.1e-222;
                                                                                                                                                                                                                                                                                                                                                       41.1%; Score 756.6; DB 12; Length 790; 98.4%; Pred. No. 2.2e-232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.5%; Score 708.4; DB 2; Length 1009; 94.7%; Pred. No. 8.6e-217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADR46580 standard; DNA; 2453 BP.
Mouse junctional adhesion molecule-1 encoding gene, SEQ ID 11.
JP2004242513-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Length 777;
                   Length 1116;
                                                                                                                                                                                    Length 790;
                                                                            AAK93330 standard; cDNA; 790 BP.
Human cDNA clone representative sequence, SEQ ID NO: 1790.
EP1130094-A2.
                                                                                                                                                                                                                                                                    5' end of a representative human cDNA cluster SeqID 1790 EP1396543-A2.
                                                                                                                                                                                    Query Match 41.1%; Score 756.6; DB 4;
Best Local Similarity 98.4%; Pred. No. 2.2e-232;
                   42.7%; Score 787; DB 12; 88.5%; Pred. No. 4.3e-242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS22474 standard; cDNA; 777 BP.
Human cDNA encoding a novel human protein #40.
WO200155437-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.7%; Score 657.4; DB 99.8%; Pred. No. 2e-200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAXX1767 standard, DNA, 726 BP.
Nucleotide sequence used to isolate DNA40628.
WO9927098-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABV83765 standard; cDNA; 1894 BP.
Human polynucleotide SEQ ID NO 94.
US2002090672-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                  ABA06428 standard; cDNA; 1894 BP.
Human cDNA SEQ ID NO: 94.
WO200154474-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX21838 standard; cDNA; 1009 BP.
                                                                                                                                                                                                                                                                                                              10-MAR-2004.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM CORP.
(ASAH-) ASAHI KASEI PHARMA CORP.
                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                               ADL29757 standard; cDNA; 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F11 antigen coding sequence. WO9902561-A1.
                                                                                                                                             05-SEP-2001.
(HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
RESULT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
ROSE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
               Query Match
Best Local Similarity
RESULT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 393
                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-AUG-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-AUG-2003
                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 394
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ADH62531 standard; DNA; 726 BP.
Human consen01 DNA used to isolate DNA40628 encoding PRO301 protein.
US2003171568-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV28137 standard; cDNA to mRNA; 1374 BP.
Mouse junctional adhesion molecule gene.
WO9824897-Al.
11.-JUN-1998.
HOFF P. HOFFWANN LA ROCHE & CO AG F.
ATY MATCH

ELocal Similarity 73.6%; Pred. No. 2e-188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.9%; Score 513.2; DB 8; Length 750; 76.9%; Pred. No. 5.7e-154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vuery Match 34.7%; Score 639; DB 12; Length 726;
Best Local Similarity 98.5%; Pred. No. 1.6e-194;
RESULT 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.7%; Score 639; DB 10; Length 726; 98.5%; Pred. No. 1.6e-194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 721;
                                     Score 639; DB 2; Length 726;
Pred. No. 1.6e-194;
                                                                                                                                                                                                       Length 726
                                                                                            ABX93346 standard; cDNA; 726 BP.
Consensus sequence expressed sequence tag, EST, consen01
US2002182206-A1.
05-DEC-2002.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.1%; Score 591.2; DB 2; 98.7%; Pred. No. 3.7e-179;
                                                                                                                                                                                                   Match 34.7%; Score 639; DB 8; Local Similarity 98.5%; Pred. No. 1.6e-194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.2%; Score 537; DB 12; 99.1%; Pred. No. 1.2e-161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADK40843 standard; cDNA; 721 BP.
DNA encoding human platelet F11 receptor #2.
US6699688-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-2004.
(UYNY ) UNIV NEW YORK STATE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADN35287 standard; DNA; 726 BP.
Human PRO301 DNA fragment consens01.
WO2004031105-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human NOVX polynucleotide #5.
WO200290504-A2.
IL4-NOV-2002.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV88991 standard; cDNA; 612 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADO08262 standard; cDNA; 750 BP.
Human NOVX polynucleotide #5.
CA (GETH ) GENENTECH INC.

Query Match
Best Local Similarity 98.5%;
RESULT 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-OCT-1998.
(GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-APR-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                    ASHKENAZI A.
                                                                                                                                                                                                                                                                                                                                                                                              GODDARD A.
GURNEY A L.
NAPIER M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity
RESULT 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WOOD W I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human NOVX polynı
US2004018594-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST clone IJ638. WO9845437-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TUMA/) TUMAS D. (WOOD/) WOOD W I
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ADH62530 standard; DNA; 390 BP.
Human DNA35936 used to isolate DNA40628 encoding PRO301 protein.
US2003171568-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX81766 standard; DNA; 390 BP.
Nuclectide sequence of DNA35936 encoding a A33 related antigen.
WG9927098-A2.
(3-JUN-1999.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                         Query Match 21.6%; Score 398.6; DB 6; Length 427; Best Local Similarity 98.6%; Pred. No. 3.4e-117; RESULT 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABQ57982 standard; cDNA; 612 BP.
Human colon cancer related nucleotide sequence SEQ ID NO:1677.
WO200229086-A2.
                                           Length 427;
                                                                                                                                                                                                     Length 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.2%; Score 390; DB 10; Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vuery Match 21.2%; Score 390; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.9e-114;
RESULT 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 21.2%; Score 390; DB 8; Length 390
Best Local Similarity 100.0%; Pred. No. 1.9e-114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABX99345 standard; cDNA; 390 BP.
Consensus assembly expressed sequence tag, EST, DNA35936.
US2002182206-Al.
                                                                                                                                                                                                                                                         ABL66995 standard, DNA, 427 BP.

Thyroid cancer related gene sequence SEQ ID NO:5332.

N W0200194629-A2.

13-200194629-A2.

13-2001.

A (AVAL-) AVALON PHARM.

21.6%; Score 398.6; DB 6; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 97.3%; Pred. No. 7.6e-117;
RESULT 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 21.6%; Score 398.6; DB 6; Best Local Similarity 98.6%; Pred. No. 3.4e-117; RESULT 411
                                       Ouery Match 21.6%; Score 398.6; DB 2; Best Local Similarity 98.6%; Pred. No. 3.4e-117; RESULT 410
                                                                                              ABL66127 standard; DNA; 427 BP.
Lung cancer related gene sequence SEQ ID NO:4464
W0200194629-A2.
13-DEC-2001.
(AVAL-) AVALON PHARM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 21.3%; Score 391.8; DB 6;
Best Local Similarity 96.3%; Pred. No. 6.7e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                 AAX56583 standard; DNA; 459 BP.
Human AA149993.RC DNA fragment.
WO9914241-A2.
    25-MAR-1999.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-DEC-2002.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-SEP-2003.
(ASHK/) ASHKENAZI A.
(FONG/) FONG S.
(GODD/) GODDARD A.
(GURN/) GURNEY A L.
(NAPI/) NAPIER M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GURNEY A L.
NAPIER M A.
TUMAS D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-APR-2002.
(FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A (TUMA/) TUMAS D.
A (WOOD/) WOOD W I.
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LUCITY MATCH STRES INST.

Best Local Similarity 97.6%; Score 492.8; DB 4; Length 605; RESULT 405

ID ADL28627 standard; CDNA; 605 BP.

E P1396543-A2.

PD 10-MAR-2004

PA (PT-RESULT 2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 27.9%; Score 513.2; DB 12; Length 750; Best Local Similarity 76.9%; Pred. No. 5.7e-154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAR-2004.

10-MAR-2004.

(REAS-) RES ASSOC BIOTECHNOLOGY.

ery Match 26.8%; Score 492.8; DB 12; Length 605;

ery Match 97.6%; Pred. No. 1.9e-147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.7%; Score 399.2; DB 2; Length 428; 98.8%; Pred. No. 2.2e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PD 25-MAR.1999.

PA (GETH ) GENENTECH INC.

Query Match

22.4%; Score 412.4; DB 2;

Best Local Similarity 93.2%; Pred. No. 1.4e-121;

RESULT 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 22.1%; Score 407.8; DB 2; Beet Local Similarity 94.7%; Pred. No. 3.9e-120; RESULT 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX56579 standard; DNA; 529 BP.
Human T86963.RC DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX56582 standard; DNA; 462 BP.
Human AA244018.RC DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAXS6563 standard; DNA; 428 BP. Human N20044.RC DNA fragment. W09914241-A2. 25-MRR-1999. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX56584 standard; DNA; 427 BP.
Human AA101562.RC DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                              (LLIUX/) LLU A. (MALY/) MALVANKAR U M. (MILL/) MILLER C B. (MILL/) MILLER I. (PADI/) PADIGARU M. (PENA/) PENA C B A. (FIEGY) RIEGER D K. (SHEN/) SHENOY S G. (SHEN/) SHENOY S G. (SHEN/) SPYTEK K A. (TAUP/) TAUPIER R J. (TAUP/) TAUPIER R J. (VOSS/) VOSS E Z. (ZERH/) ZERHUSEN B D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-1999.
(GETH ) GENENTECH INC.
BOLDOG F L.
BURGESS C E.
CASMAN S J.
CHAPOVAL A.
EDINGER S R.
GERLACH V.
GORMAN L.
GUNTHER E.
                                                                                                                                                          GUO X S.
KEKUDA R.
LEPLEY D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity
RESULT 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                           CHAP/)
EDIN/)
                                                                                                                     GORM/)
                                                                                                                                                          (GUOX/)
                                                                                                                                                                                                                                        rinx/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 404
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Best Local Similarity 100.0%; Pred. No. 7.2e-112; RESULT 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 431
ID ABS56664 standard; cDNA; 382 BP.
DB Prostate tumour cDNA #135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MCNEILL P D.
HOUGHTON R L.
Y DE BASSOLS C V.
FOY T M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) KELKY Y A W.
) HEPLER W T.
) HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                           LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HENDERSON R A. HURAL J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
LI S X.
WANG A.
                                                                                17-MAY-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                             STOLK J A.
DAY C H.
VEDVICK T S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DILLON D C.
MITCHAM J L.
HARLOCKER S 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                              MITCHAM J L.
HARLOCKER S
                                                                                                                                                                                                                                                                                            JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
                                                                                                                                                                                                                                  XU J.
DILLON D C.
                                                                                                                           Best Local Similarity
RESULT 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FANGER G R. RETTER M W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JIANG Y.
KALOS M D.
                                                                                                                                                                                                                                                                                                                                                                                                            CARTER D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human P185 cDNA
US2002022248-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-200
                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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(FOYT/)
                                                                                                                                                                                                                                                                                              (JIAN/)
(KALO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HEPL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HEND/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LISX/
                                                                                                                                                                                                                                                                               HARL/
                                                                                                                                                                                                                                                                                                                                                                                                                             LISX/
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                                                                                                                                                                                                                                (XOO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKEI/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HURA/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DILL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAO6375 standard; cDNA; 382 BP.
Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:139.
WC200004149-A2.
                                                                                                                                                                                                                                             Length 387;
                                                                                     15-ARK-ZUUY.
(GETH ) GENENTECH INC.
:ry Match 21.2%; Score 390; DB 12; Length 390;
:r Local Similarity 100.0%; Pred. No. 1.9e-114;
                                                                                                                                                                                                                                                                                                                                                                         20.7%; Score 382; DB 2; Length 382; 100.0%; Pred. No. 7.2e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.7%; Score 382; DB 4; Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH02556 standard; cDNA; 382 BP.
Prostate tumour antigen determined cDNA sequence for P185.
WO200125272-A2.
12-APR-2501.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human prostate tumour protein partial DNA sequence #131.
US2002090372-A1.
                                                                                                                                                                                                  MUSALAL.-
25-MAR-1999.
25-MAR-1999.
GETY MATCh 20.9%; Score 384.4; DB 2;
ery Match 20.9%; Pred. No. 1.2e-112;
 100.0%; Pred. No. 1.9e-114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.7%; Score 382; DB 3; I 100.0%; Pred. No. 7.2e-112;
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100.0%; Pred. No. 7.2e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH93491 standard; cDNA; 382 BP.
Human prostate-specific cDNA sequence P185.
WO200151633-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                      AAV61227 standard; cDNA; 382 BP. cDNA sequence of prostate tumour clone. WO9837093-A2.
                                                                                                                                                                                                                                                                                         AAV58612 standard; cDNA; 382 BP.
Prostate tumour specific gene clone.
WO9837418-A2.
                              ADN35286 standard; DNA; 390 BP.
Human PRO301 DNA fragment DNA35936.
WO2004031105-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS63583 standard; cDNA; 382 BP.
Human prostate cDNA sequence #135.
WO200173032-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABS71280 standard; cDNA; 382 BP.
                                                                                                                                                             AAX56535 standard; DNA; 387 BP.
Human AA152150 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                      PD 27-AUG-1998.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1
RESULT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2-A2.
2001.
201.
2ry Match
Best Local Similarity DRESULT 426
ID AAH02556 stande
DB Prostate transported by WO2001?
PD 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-AUG-1998.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JAN-2000.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUL-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
RESULT 422
                                                                                                                                                                                                                                                         Best Local Similarity RESULT 420
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Best Local Similarity
RESULT 424
Best Local Similarity RESULT 418
                                                                                                                             Best Local Similarity RESULT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DILL/) DILLON D C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
RESULT 425
                                                                                  15-APR-2004
                                                                                                                Query Match
                                                                                                                                                                                                                                             Query Match
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20.7%; Score 382; DB 4; Length 382; 100.0%; Pred. No. 7.2e-112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.7%; Score 382; DB 5; Length 382; 100.0%; Pred. No. 7.2e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 382; DB 6; Length 382;
Pred. No. 7.2e-112;
                                                                                                                                                                                                                                              Prostate cancer therapy associated cDNA #135.
US2002192763-A1.
19-DBC-2002.
AAH84805 standard; cDNA; 382 BP.
Human prostate-specific cDNA sequence P185.
WO200134802-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL94955 standard; cDNA; 382 BP.
Human P185 cDNA sequence SEQ ID NO 139
                                                                                                                                                                                                                       ACA59392 standard; cDNA; 382 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS10134 standard; cDNA; 382 BP.
Human prostate tumour cDNA #25.
US6262245-B1.
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WO9914241-A2.
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                                           Query Match
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cDNA encoding human skin cell transmembrane protein, SEQ ID NO:54.
WO9955865-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-NOV-2001.
(GENE-) GENESIS RES & DEV CORP LTD.
ery Match 20.7%; Score 380.4; DB 6; Length 403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.7%; Score 380.4; DB 4; Length 403; 99.7%; Pred. No. 2.4e-111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.3%; Score 373.2; DB 2; Length 467; 97.0%; Pred. No. 5.6e-109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-NOV-1999.
(GENE-) GENESIS RES & DEV CORP LTD.
ery Match
ery Match
-- Tocal Similarity 99.7%; Pred. No. 2.4e-111;
                                                                                                                                                                                                                                                                                                         20.7%; Score 382; DB 10; Length 382; 100.0%; Pred. No. 7.2e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 415;
                                                                                                                                                                                   20.7%; Score 382; DB 8; Length 382; 100.0%; Pred. No. 7.2e-112;
                                                            Length 382;
                                                                                                        ACC95119 standard; cDNA; 382 BP.
Prostate tumour specific cDNA sequence SEQ ID 139.
WO200289747-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL34744 standard; cDNA; 403 BP.
Human cDNA isolated from skin cells SEQ ID NO: 54
WO200190357-A1.
                                                           20.7%; Score 382; DB 6; Lo
100.0%; Pred. No. 7.2e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                   20.7%; Score 382; DB 10; 100.0%; Pred. No. 7.2e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUDALINE 1999.
25-MAR-1999.
GUERY MATCH 20.5%; Score 378; DB 2; I 20ery Match 20.5%; Pred. No. 1.5e-110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-NOV-2000.
(GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                   ADG26005 standard, CDNA, 382 BP.
Human prostate-specific CDNA #135.
21-AUG-2003.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                ADB13589 standard; cDNA; 382 BP.
Human prostate specific cDNA P185.
US2003185830-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC99592 standard; cDNA; 403 BP.
Skin cell cDNA, SEQ ID NO: 54.
WO200069884-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX56542 standard; DNA; 467 BP.
Human N28398 DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX56502 standard; DNA; 395 BP.
Human W76302 DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX56510 standard; DNA; 415 BP.
Human AA101561 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-1999.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
IRSULT 434
ID AGG26005 standard; CDR
DE Human prostate-specifi
PN US203157089-A1.
PD 21-AUG-2003.
PA (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
RESULT 432
                                                                                                                                                   14-NOV-2002.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
RESULT 437
                                                                                                                                                                                                                                                                            02-OCT-2003.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
RESULT 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 439
            27-JUN-2002.
(XUJJ/) XU J.
(DILL/) DILLON D C.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
RESULT 435
                                                                                                                                                                                                Best Local Similarity RESULT 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 440
 US2002081580-A1.
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                                                                                                                                                                                    Query Match
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AAH87415 standard; DNA; 327 BP.
Human single nucleotide polymorphism containing DNA sequence #2272.
WO9953095-A2.
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Human single nucleotide polymorphism containing DNA sequence #454.
WO9953095-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AALO0711 standard; cDNA; 425 BP.

Human reproductive system related antigen cDNA SEQ ID NO: 712.
W0200155320-A2.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WOOT-1999.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.

ery Match 17.6%; Score 323.8; DB 2; Length 327;

ery Match 199,4%; Pred. No. 3.7e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PD 21-OCT-1999.

PA (WHED) WHITEHEAD INST BIOMEDICAL RES.

Query MAtch 17.6%; Score 323.8; DB 2; Length 327;

Best Local Similarity 99.4%; Pred. No. 3.7e-93;

RESULT 447
                                                                                                                                                                                                                                                                                                                                                                                           Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.4%; Score 320.8; DB 4; Length 425; 98.5%; Pred. No. 4e-92;
                                                                                                                                                                                                                    DB 2; Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 425;
                                        Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PD 25-MAR-1999.

PA (GETH) GENENTECH INC.

Query Match

18.0%; Score 330.8; DB 2;

Query Match

18.0%; Pred. No. 2.2e-95;

RESULT 444

ID ACH30092 standard; CDNA; 416 BP.
                                                                                                                                                                                                                                                                                                                                                                           Uuery Match
18.2%; Score 335.6; DB 2;
Best Local Similarity ' 96.4%; Pred. No. 7.6e-97;
RESULT 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                        19.2%; Score 354; DB 2; I
99.5%; Pred. No. 7.7e-103;
                                                                                     ID AAX56574 standard; DNA; 341 BP.

DE Human T40695.RC DNA fragment.

DN W0991441-A2.

PD 25-MAR-1999.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 99.4%; Pred. No. 1.2e-97;

RESULT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.9%; Score 330; DB 9; 95.6%; Pred. No. 4.3e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.4%; Score 320.8; DB 98.5%; Pred. No. 4e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS28818 standard; cDNA; 425 BP.
Human immunoglobulin encoding cDNA SEQ ID No W020015315-A2.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                 AAX56577 standard; DNA; 503 BP.
Human R72982 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX56559 standard; DNA; 358 BP.
Human AA483522.RC DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DE Human testis cDNA #478.

PN US2003073623-A1.

PA (DRWA/) DRWANAC R T.

PA (LABA/) LABAT I.

PA (STRC/) STACHS-CRAIN B.

PA (DRCK/) DICKSON M C.

OUCEY/ MATCH
25-MAR-1999.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                25-MAR-1999.
(GETH ) GENENTECH INC.
                                                      Best Local Similarity RESULT 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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Best Local Similarity 87.4%; Pred. No. 3e-85;
                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DS.C.2.7003.
24-APR-2003.
(HUMA-) HUMAN GENOME SCI INC.
ery Match
17.4%; Score 320.8; DB 10; Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-MAR-2003.
(HUMA-) HUMAN GENOME SCI INC.
ery Match
17.4%; Score 320.8; DB 11; Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) 25-MAR-1999.
A (GETH ) GENENTECH INC.
Query Match 16.3%; Score 299.6; DB 2; Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PD 25-MAR-1999.

PA (GETH ) GENENTECH INC.

Query Match 17.4%; Score 320.4; DB 2; Length 322;

Best Local Similarity 99.7%; Pred. No. 4.6e-92;

RESULT 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Query Match 16.8%; Score 310.2; DB 2; Length 435;
Best Local Similarity 97.2%; Pred. No. 1.1e-88;
RESULT 457
                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
ry Match
t Local Similarity 98.5%; Pred. No. 4e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.4%; Score 320.8; DB 6; Length 425; 98.5%; Pred. No. 4e-92;
                                                                                                                  Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 17.3%; Score 318; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 3.1e-91;
RESULT 456
                                                                                                                                                                     AAS40130 standard; cDNA; 425 BP.
DNA encoding human prostate cancer antigen, Seq ID No 71
W0200155316-A2.
02-ANG-2001.
                                                                   OZ-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
(HTWA-) HUMAN 17.4%; Score 320.8; DB 4;

LT.4%; Pred. No. 4e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADB31543 standard; cDNA; 425 BP.
Human cDNA encoding a novel protein SEQ ID NO 64.
US2003077606-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human prostate cancer associated gene SeqID71 US2003054373-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABV42676 standard; cDNA; 394 BP.
Human prostate expression marker cDNA 42667.
WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                 ABV83787 standard; CDNA; 425 BP.
Human polynucleotide SEQ ID NO 116.
US200209672-A1.
11-JUL-2002.
                ABA06450 standard; cDNA; 425 BP.
Human cDNA SEQ ID NO: 116.
WO200154474-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA; 322 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX56552 standard; DNA; 504 BP.
Human AA224590.RC DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA; 435 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADJ09125 standard; DNA; 425 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX56529 standard; DNA; 32
Human 979636 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX56524 standard; DNA; 45
Human T87045 DNA fragment.
WO9914241-A2.
                                          --A2.

--A4.) HUMAN GENOM.

--GTY MATCh

Best Local Similarity 5
RESULT 450
ID AAS40130 stand>
DE DNA encodir
PN WO20015
PP 02
                                                                                                                                                                                                                                                                                          Best Local Similarity
RESULT 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 454
                                                                                                                                                                                                                                                                                                                                                                                                               (RUBE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
RESULT 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
RESULT 449
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Query Match 15.5%; Score 286.4; DB 6; Length 1009; Best Local Similarity 73.2%; Pred. No. 8.3e-81;
                                                 PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 299.2; DB 2; Length 408;
Best Local Similarity 91.0%; Pred. No. 3.6e-85;
RESULT 459
                                                                                                                                                                                                                                               GETH ) GENENTECH INC. (GETH ) GENENTECH INC. ery Match 15.8%; Score 291.4; DB 2; Length 296; ery Match Similarity 98.6%; Pred. No. 9.7e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PD 25-WAR-1999.

PA (GETH ) GENENTECH INC.

Query Match

15.4%; Score 284.4; DB 2; Length 286;

Best Local Similarity 99.7%; Pred. No. 1.7e-80;

RESULT 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 15.5%; Score 285.8; DB 2; Length 289; Local Similarity 99.3%; Pred. No. 6.1e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.2%; Score 280.4; DB 2; Length 282; 99.6%; Pred. No. 3.3e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          PA (GETH ) GENENTECH INC.
QUERY MAtch
15.8%; Score 291; DB 2; I
Best Local Similarity 100.0%; Pred. No. 1.3e-82;
RESULT 46.
ID AAX37719 standard; DNA; 293 BP.
DE Human clone T87045 DNA.
PN W09914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 15.3%; Score 281; DB 2; Best Local Similarity 100.0%; Pred. No. 2.1e-79; RESULT 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 291; DB 2;
Pred. No. 1.3e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABN74213 standard; cDNA; 1009 BP.
Bovine embryonic germ (EG) cell cDNA EST #264.
W0200194550-A2.
(INPL-) INPIGEN INC.
AAX56587 standard; DNA; 408 BP.
Human R01692.RC DNA fragment.
W09914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX56566 standard; DNA; 286 BP.
Human 3212856 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                  AAX56554 standard; DNA; 296 BP.
Human 930239 DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX56532 standard; DNA; 281 BP.
                                                                                                                                                                                                                                                                                                                                                                       AAX56539 standard; DNA; 291 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA; 282 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
ry Match 15.8%;
t Local Similarity 99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 463
ID AAX56572 standard; DNA; 289
                                                                                                                                                                                                                                                                                                                                                                                          Human 1818676 DNA fragment.
WO9914241-A2.
25-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human 2925803 DNA fragment WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX56576 standard; DNA; 282
Human 3144865 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human 1793273 DNA fragment WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-1999.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
                                                                                                                                                                                                                                 WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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PD 25-MAR-1999.

PA (GETH ) GENENTECH INC.

QUETY MATCh 15.2%; Score 279.8; DB 2; Length 378;

Best Local Similarity 91.1%; Pred. No. 6.1e-79;

RESULT 468
                                                                                                                                                                                                                                                                                                                                                                                 PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 14.9%; Score 273.6; DB 2; Length 528;
Best Local Similarity 79.7%; Pred. No. 7.5e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 14.8%; Score 273.4; DB 2; Length 287;
Best Local Similarity 99.3%; Pred. No. 6e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PD 25-MAR-1999.
AA (GETH ) GENENTECH INC.
Query Match 14.5%; Score 267.4; DB 2; Length 269;
Best Local Similarity 99.6%; Pred. No. 4.9e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 14.2%; Score 260.8; DB 2; Length 264; Best Local Similarity 99.2%; Pred. No. 6.5e-73; RESULT 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 14.1%; Score 260; DB 2; Length 260; Best Local Similarity 100.0%; Pred. No. 1.2e-72; RESULT 476
                                                                                                                                                                                                                                                                                   Query Match 14.9%; Score 275; DB 2; Length 275; Best Local Similarity 100.0%; Pred. No. 1.8e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 261;
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25-MAR-1999.
(GETH ) GENENTECH INC.
(ery Match
14.2%; Score 261; DB 2; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PD 25-MAR.1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 99.6%; Pred. No. 3.2e-75;
                                                                                                                                                                              AAX56538 standard; DNA; 275 BP. Human 956595 DNA fragment. w09914241-A2. 25-MAR-1999. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX56531 standard; DNA; 269 BP.
Human 2328920 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX56562 standard; DNA; 264 BP.
Human 1283885 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX56517 standard; DNA; 260 BP. Human 3236257 DNA fragment. wO9914241-A2. 25-MAR-1999. (GETH ) GENENTECH INC.
                 AAX56590 standard; DNA; 378 BP.
Human T84017.RC DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX56565 standard; DNA; 287 BP.
Human 2025350 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX56557 standard; DNA; 269 BP.
Human 1004380 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX56522 standard; DNA; 261 BP.
Human 1731885 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                 DNA; 528 BP.
                                                                                                                                                                                                                                                                                                                                           AAX56570 standard; DNA; 528
Human AA244075 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-1999.
(GETH ) GENENTECH INC.
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RESULT 467
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PD 25-MAR-1999.

PA (GETH ) GENENTECH INC.

QUERY MATCh

Best Local Similarity 99.6%; Pred. No. 1.6e-70;

RESULT 482

ID AAXS6514 standard; DNA; 252 BP.

PN W09914241-A2.

PD 25-MAR-1999.

PA (GETH ) GENENTECH INC.

QUERY MATCh

Best Local Similarity 100.0%; Pred. No. 4.4e-70;

RESULT 483
                                                                                                                                                                                                                                                                                                          ..., GENENTECH INC.

Julery Match

Best Local Similarity 100.0%; Pred. No. 1.1e-71;

RESULT 479

ID AAX56573 standard; DNA; 256 BP.

PDE Human 145563 DNA fragment.

PN W09914241-A2.

PD 25-WAR-190°
ID AAX56589 standard; DNA; 274 BP.

DE Human AA.101520.RC DNA fragment.

PN W09914241-92.

PD 25-WAR-1999.

PA (GETH ) GENENTECH INC.

Query Match

14.0%; Score 258.4; DB 2; Length 274;

RESULT 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DE Human 1345563 DNA fragment.
PW W09914241-A2.
PD 2-MAR-1999.
PA (GETH ) GENENTECH INC.
QUETY MATCh
Best Local Similarity 99.64; Pred. No. 7.4e-71; RESULT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 13.8%; Score 254.4; DB 2; Length 256; Best Local Similarity 99.6%; Pred. No. 7.4e-71; RESULT 481
                                                                                                                                                                                                                PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 258; DB 2; Length 271;
Best Local Similarity 99.6%; Pred. No. 5.3e-72;
RESULT 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAXI1439 standard; DNA; 251 BP.
Human biallelic polymorphic DNA fragment WI-8024c.
WO9820165-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.7%; Score 252; DB 2; I 100.0%; Pred. No. 4.4e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX56558 standard; DNA; 256 BP.
Human 1211411 DNA fragment.
W09914241-A2.
25-MRR-1999.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX56569 standard; DNA; 255 BP.
Human 1804959 DNA fragment.
WO9914241-A2.
                                                                                                                                                                         AAX56503 standard; DNA; 271 BP.
Human 3124762 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX56507 standard; DNA; 257 BP.
Human 1298110 DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09914241-A2.
25-MAR-1999.
(GETH ) GENENTECH INC.
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RESULT 484
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WO9914241-A2.
                                                                                                                                                                                                             PD 25-MAR-1999.

PA (GETH) GENENTECH INC.

QUETY MATCh

13.6%; Score 250.4; DB 2; Length 252;

BBSt Local Similarity 99.6%; Pred. No. 1.4e-69;

RESULT 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 13.5%; Score 247.8; DB 2; Length 252; Best Local Similarity 98.8%; Pred. No. 9.8e-69; RESULT 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.4%; Score 247.4; DB 2; Length 257; 96.5%; Pred. No. 1.3e-68;
                                                                                             Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 250;
                          PD 14-MAY-1998.

PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.

Query Match 13.6%; Score 250.6; DB 2;

Best Local Similarity 99.6%; Pred. No. 1.2e-69;

RESULT 486
                                                                                                                                                                                                                                                                                                                          DE Human 014756 DNA fragment.

PN W0914241-A2.

PN W0914241-A2.

PN W0914241-A2.

PN W0914241-A2.

PN W0914241-A2.

PN W0914241-B2.

PN W0914241-B2.

Query Match

Best Local Similarity 96.0%; Pred. No. 1.9e-69;

RESULT 488

DE Human 2345419 DNA fragment.
Human biallelic polymorphic DNA fragment WI-8024b. WO9820165-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PD 25-MAR-1999.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 98.4%; Pred. No. 2.6e-69;

RESULT 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH) GENENTECH INC.

ry Match

13.6%; Score 250; DB 2; I

t Local Similarity 100.0%; Pred. No. 1.9e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.6%; Score 250; DB 2; Best Local Similarity 100.0%; Pred. No. 1.9e-69; RESULT 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 97.1%; Pred. No. 2.4e-69;
RESULT 491
                                                                                                                                                     AAX56555 standard; DNA; 252 BP.
Human 876764 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX56513 standard; DNA; 257 BP.
Human 492141 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX37718 standard; DNA; 250 BP.
Human clone 2345419 DNA.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX56547 standard; DNA; 360 BP.
Human R28222 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA; 256 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX56519 standard; DNA; 247 BP.
Human 1452523 DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX56525 standard; DNA; 252
Human 1932979 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX56509 standard; DNA; 256
Human 2197534 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-1999.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENENTECH INC.
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Best Local Similarity
RESULT 494
ID AAX56519 standard; DN
DE Human 1452523 DNA fra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9914241-A2.
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Score 239.4; DB 2; Length 241; Pred. No. 4.9e-66;
                                                                                                                                          PD 25-MAR-1199.

PA (GETH ) GENENTECH INC.

Query Match

Best Local Similarity 98.0%; Pred. No. 2.4e-68;

RESULT 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PD 25-MAR-1999.

AA (GETH ) GENENTECH INC.

Query Match

13.2%; Score 242.4; DB 2; Length 256;

Beet Local Similarity 99.2%; Pred. No. 5.4e-67;

RESULT 499
                                                                                                                                                                                                                                                                                                                                                  Query Match 13.3%; Score 245.4; DB 2; Length 248; Best Local Similarity 99.2%; Pred. No. 5.8e-68; RESULT 497
                  query Match 13.4%; Score 247; DB 2; Length 247; Best Local Similarity 100.0%; Pred. No. 1.8e-68; RESULT 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 12.9%; Score 237; DB 2; Length 237; Best Local Similarity 100.0%; Pred. No. 2.9e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH') GENENTECH INC.
ry Match
13.0%; Score 240; DB 2; L
t Local Similarity 100.0%; Pred. No. 3.1e-66;
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(GETH) GENENTECH INC.
(ery Match 13.2%; Score 244; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 240; DB 2;
Pred. No. 3.3e-66;
                                                                                                                                                                                                                                                        AAX56585 standard; DNA; 248 BP.
Human 2223391 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX56560 standard; DNA; 256 BP.
Human 732999 DNA fragment.
WO9914241-A2.
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Human 1807742 DNA fragment.
WO9914241-A2.
                                                                                           AAX56581 standard; DNA; 255 BP.
Human 647074 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                      DNA; 245 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX56506 standard; DNA; 259 BP.
Human 3234064 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAXS6537 standard; DNA; 237 BP. Human 1274809 DNA fragment. WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX56544 standard; DNA; 240 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 503
ID AAX56561 standard; DNA; 240 BP.
DE Human 1282058 DNA fragment.
PN W09914241-A2.
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(GETH) GENENTECH INC.
13.0%;
Query Match 13.0%;
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A (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 99.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                AAX56540 standard, DNA, 245
Human 2220993 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human 3240004 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                  25-MAR-1999.
(GETH ) GENENTECH INC.
25-MAR-1999.
(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity RESULT 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
RESULT 500
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(GETH ) GEN
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AAX56508 standard; DNA; 243 BP.
Human AA101519 DNA fragment.
WO9914241-A2.
25-WAR-1999.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
Ery Match
St Local Similarity 96.6%;
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Human AA215609 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-SEP-2001.
(HELI-) HELIX RES INST.
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(GETH ) GENENTECH INC.
                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9914241-A2.
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Best Local Si
RESULT 517
                                                                                                                                                                                                                                                                               AAX56550 standard; DNA; 264 BP.

Human T39606 DNA fragment.

W09914441-A2.
25-MAR-1999.

(GETH ) GENENTECH INC.

12.5%; Score 230.8; DB 2; Length 264; Bt Local Similarity 95.2%; Pred. No. 3e-63;
PD 25-MAR-1999.

PA (GETH) GENENTECH INC.

Query Match 12.9%; Score 236.8; DB 2; Length 240;

Best Local Similarity 99.2%; Pred. No. 3.3e-65;

RESULT 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Query Match
12.5%; Score 230.4; DB 2; Length 232;
Best Local Similarity 99.6%; Pred. No. 3.8e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uuery Match
12.2%; Score 224.4; DB 2; Length 226;
Best Local Similarity 99.6%; Pred. No. 3.2e-61;
RESULT 509
                                                                                                                                                                                                                            12.6%; Score 232.6; DB 2; Length 268; 92.6%; Pred. No. 8.1e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-62;
RESULT 508

ID AAX56564 standard; DNA; 226 BP.
DE Human 2797137 DNA fragment.
PD WO9914241-A2.
PD 55-MAR-1999.
PA (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PD 25-MAR-1999.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 100.0%; Pred. No. 4.3e-61;

RESULT 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 82.5%; Pred. No. 1.3e-60; RESULT 512
ID AAX37720 standard; DNA; 220 BP.
PN W09914241-A2
PD 25-Wr-
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PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 8.9e-61;
RESULT 511
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX56586 standard; DNA; 232 BP.
Human 1447744 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX56541 standard; DNA; 224 BP.
Human 1706515 DNA fragment.
WO9914241-A2.
                                                                                                                         AAX56505 standard; DNA; 268 BP.
Human 777818 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX56511 standard; DNA; 227 BP.
Human AA227408 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX56580 standard; DNA; 223 BP.
Human 767739 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX56528 standard; DNA; 430 BP.
Human R02633 DNA fragment.
W09914241-A2.
                                                                                                                                                                                      25-MAR-1999.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                        Best Local Similarity
RESULT 505
                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
RESULT 506
                                                                                                                                                                                                                              Ouery Match
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vuery Match 11.7%; Score 215.6; DB 12; Length 581; Best Local Similarity 82.9%; Pred. No. 3.9e-58; RESULT 519
                                                                                                                                                                                                                                                                                                                        PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 11.9%; Score 219.4; DB 2; Length 271;
Best Local Similarity 94.6%; Pred. No. 1.5e-59;
RESULT 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 11.7%; Score 215.6; DB 4; Length 581; Best Local Similarity 82.9%; Pred. No. 3.9e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PD 25-WAR-1999.

PA (GTH) GENENTECH INC.

Query Match 11.8%; Score 217; DB 2; Length 235;

Best Local Similarity 96.6%; Pred. No. 7.9e-59;

RESULT 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PD 25-MRA-1999.

PA (GETH) GENENTECH INC.

Query Match

11.6%; Score 213; DB 2; Length 236;

Best Local Similarity 98.2%; Pred. No. 1.5e-57;

RESULT 521
                                                                                                                                                     PD 25-WAR-1999.

PA (GETH ) GENENTECH INC.

11.9%; Score 220; DB 2; Length 220; Beet Local Similarity 100.0%; Pred. No. 8.2e-60; RESULT 514

ID AAX56575 standard; DNA; 271 BP.

DE Human R27969.RC DNA fragment.

PN 909914241-A2.
Query Match 11.9%; Score 220; DB 2; Length 220; Best Local Similarity 100.0%; Pred. No. 8.2e-60; RESULT 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 216.2; DB 2;
Pred. No. 1.4e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cuery Match 11.7%; Score 215; DB 2;
Best Local Similarity 96.0%; Pred. No. 3.7e-58;
RESULT 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAK92951 standard; cDNA; 581 BP.
Human cDNA 3'-end sequence, SEQ ID NO: 1411.
EP1130094-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADL29378 standard; cDNA; 581 BP.
3' end of a human cDNA molecule SeqID 1411.
EP1396543-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                            AAX56526 standard; DNA; 220 BP.
Human 1508565 DNA fragment.
WO9914241-A2.
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Human 2044611.RC DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX56556 standard; DNA; 239 BP.
Human 159097 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX56553 standard; DNA; 235 BP.
Human 929944 DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA; 262 BP.
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76.1%; Pred. No. 8.2e-52;

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Best Local Similarity RESULT 531
                                                                                                                                                                                                                                                                                        vuery Match
11.2%; Score 206.8; DB 2; Length 234;
Best Local Similarity 98.3%; Pred. No. 1.5e-55;
RESULT 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-WAR-1999.
(GETH ) GENENTECH INC.
ery Match 10.9%; Score 201.4; DB 2; Length 203;
ery Match 99.5%; Pred. No. 7.7e-54;
Query Match 11.4%; Score 209.2; DB 2; Length 243; Best Local Similarity 96.7%; Pred. No. 2.6e-56; RESULT 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                vuery Match
Best Local Similarity 87.8%; Pred. No. 4.8e-54;
RESULT 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HDMA-) HUMAN GENOME SCI INC.

17 Match 10.6%; Score 195.6; DB 4; Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 403;
                                                                                                                                                     Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-SEP-2001.
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
ery Match 10.9%; Score 200.2; DB 5;
ery match 98.1%; Pred. No. 2.2e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC. 10.9%; Score 200.2; DB 5; t Local Similarity 98.1%; Pred. No. 2.2e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS28795 standard; cDNA; 367 BP.
Human immunoglobulin encoding cDNA SEQ ID No 41.
WO200155315-A2.
                                                                                                              ) 25-MAR-1999.

A (GETH ) GENENTECH INC.

Query Match 11.2%; Score 207; DB 2;

Best Local Similarity 99.5%; Pred. No. 1.3e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.8%; Score 198.4; DB 4 94.9%; Pred. No. 1.1e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADL38773 standard; DNA; 263 BP.
Human ovarian cancer DNA marker #12663.
WO200170979-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADL45157 standard; DNA; 517 BP.
Human ovarian cancer DNA marker #19047.
WO200170979-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADI73644 standard; DNA; 263 BP.
Human ovarian cancer DNA marker #6386.
WO200170979-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI91738 standard; cDNA; 403 BP.
Human polynucleotide SEQ ID NO 11798.
WO200164835-A2.
                                                       AAX56546 standard; DNA; 219 BP.
Human 2382718 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                           AAX56549 standard; DNA; 234 BP.
Human T39607 DNA fragment.
                                                                                                                                                                                                                                                                                                                                                               AAX56523 standard; DNA; 396 BP.
Human T84016 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA; 203 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX56567 standard; DNA; 203
Human 1611708 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                              25-MAR-1999.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 526
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Best Local Similarity
RESULT 527
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RESULT 528
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(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                  WO9914241-A2.
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ID AAI9173
DE Human F
PN WO20016
PD 07-SEP-
                                                                                                                                                                                         RESULT 523
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AAL02302 standard; cDNA; 367 BP.
Human reproductive system related antigen cDNA SEQ ID NO: 2303.
WO200155320-A2.
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                                                                                                       10.6%; Score 195.6; DB 4; Length 367; 76.1%; Pred. No. 8.2e-52;
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                                                                                                                                                                                                                                                                          4; Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 205;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 194.8; DB 2;
Pred. No. 1e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-1999.
(GETH ) GENENTECH INC.
PRY MATCH 10.6%; SCORE 194.4; DB 2;
it Local Similarity 93.6%; Pred. No. 1.8e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.6%; Score 195.6; DB 6; 76.1%; Pred. No. 8.2e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cDNA encoding a novel protein SEQ ID NO 41.
US2003077606-A1.
24-APR-2003.
                                                                                                                                                                                                                                                                     10.6%; Score 195.6; DB 4 76.1%; Pred. No. 8.2e-52;
                                                                                                                                                                                                                                                                                                                     Human polynucleotide SEQ ID NO 324. US2002090672-A1.
                                                                                                                                                                ABA06658 standard; cDNA; 367 BP.
Human cDNA SEQ ID NO: 324.
WO200154474-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADB31520 standard; cDNA; 367 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX56501 standard; DNA; 303 BP.
Human C17760 DNA fragment.
WO9914241-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX56536 standard; DNA; 198 BP.
Human 1610836 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX37717 standard; DNA; 297 BP.
Human clone 1452523 DNA.
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25-WAR-1999.
(GETH ) GENENTECH INC.
Watch ....ttv 99.0%;
                                                                                   (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
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WO9914241-A2.
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Human 1508552 DNA fragment
WO9914241-A2.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                           11-JUL-2002.
(ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                   Best Local Similarity
RESULT 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
RESULT 536
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                                                                02-AUG-200
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Query Match 9.8%; Score 179.6; DB 2; Length 201; Best Local Similarity 91.5%; Pred. No. 8.1e-47; RESULT 542
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(GETH ) GENENTECH INC.
7.8%; Score 144.4; DB 2; Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 203;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vuery Match 8.6%; Score 158.4; DB 2; Length 274;
Best Local Similarity 95.9%; Pred. No. 6.6e-40;
RESULT 547
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Best Local Similarity 100.0%; Pred. No. 8.3e-43;
RESULT 543
ID AAX56548 standard; DNA; 203 BP.
DE Human 1889866 DNA fragment.
PN WO9914241-42.
PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
         10.2%; Score 187; DB 2; Length 297; 83.2%; Pred. No. 4.2e-49;
                                                                                                                                                         Length 186;
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                                                                                              PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 10.1%; Score 186; DB 2; 1
Best Local Similarity 100.0%; Pred. No. 6.7e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 8.9%; Score 163.2; DB 2.
Best Local Similarity 92.7%; Pred. No. 1.6e-41;
RESULT 544
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Best Local Similarity 84.8%; Fred. No. 2.2e-38;
RESULT 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX56534 standard; DNA; 204 BP.
Human 1521745 DNA fragment.
WO9914241-A2.
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Human 1519947 DNA fragment.
WO9914241-A2.
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Human 2861301 DNA fragment.
WO9914241-A2.
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Human T73746 DNA fragment.
WO9914241-A2.
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Human 241604 DNA fragment.
WO9914241-A2.
                                                           AAX56591 standard; DNA; 186 BP.
Human 1208791 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                         AAX56543 standard; DNA; 201 BP.
Human 360948 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                         AAX56530 standard; DNA; 167 BP.
Human AA404390 DNA fragment.
WO9914241-A2.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
Query Match
Best Local Similarity
RESULT 540
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Best Local Similarity
RESULT 545
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ABL97457 standard; DNA; 4067 BP.
Human testicular antigen encoding DNA fragment SEQ ID NO: 2109.
WO200155317-A2.
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WO200155317-A2.
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PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 6.8%; Score 124.4; DB 5; Length 447;

Best Local Similarity 85.2%; Pred. No. 8.1e-29;

RESULT 552
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Human reproductive system related antigen DNA SEQ ID NO: 7222
WO200155320-A2.
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Human reproductive system related antigen DNA SEQ ID NO: 7225
WO200155320-A2.
                                                                                                                                                                                                                                                                                                                              Score 132.6; DB 2; Length 141; Pred. No. 9.1e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 265;
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(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
ery Match
for Index B 5;
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Best Local Similarity 100.0%; Pred. No. 6.3e-26;
RESULT 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vuery Match 6.4%; Score 118; DB 2;
Best Local Similarity 91.3%; Pred. No. 5.4e-27;
RESULT 553
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PA (HUMA-) HUMAN GENOME SCI INC.

Query Match

6.2%; Score 115; DB 4;

Best Local Similarity 80.5%; Pred. No. 3.3e-25;

RESULT 56
Best Local Similarity 98.6%; Pred. No. 1.5e-35; RESULT 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 6.2%; Score 115; DB 4;
Local Similarity 80.5%; Pred. No. 3.3e-25;
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HUMA-) HUMAN GENOME SCI INC.
PY MATCH 6.2%; Score 115; DB 4;
St Local Similarity 80.5%; Pred. No. 3.3e-25;
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Best Local Similarity 85.2%; Pred. No. 5.9e-
RESULT 55.1
ID ANY 2650 standard; CDNA; 447 BP.
DE Human prostate expression marker CDNA 12641.
PN WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABV33780 standard; cDNA; 265 BP.
Human prostate expression marker cDNA 33771.
WO200160860-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX56593 standard; DNA; 180 BP.
Human 143613 DNA fragment.
WO9914241-A2.
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(HUMA-) HUMAN GENOME SCI INC.
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(GETH ) GENENTECH INC. 7, 2%;
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(HUMA-) HUMAN GENOME SCI INC.
                                                                                                               AAXS6512 standard; DNA; 141
Human 2612024 DNA fragment.
WO9914241-A2.
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(GETH ) GENENTECH INC.
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RESULT 550
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Best Local Similarity
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AAK78375 standard; DNA; 6780 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33187.
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                        Length 110000;
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                                             Score 113.4; DB 6; Length 110000;
Pred. No. 8.2e-24;
                                                                                                   Length 110000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 113.2; DB.10; Length 78313; Pred. No. 7.7e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 113.2; DB 9; Length 78313; Pred. No. 7.7e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Length 2522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 6780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human FYN carcinoma associated gene, SEQ ID NO:1136
WO2003057146-A2.
                                                                                                                                                      Score 113.4; DB 12;
Pred. No. 8.2e-24;
                                                                                                                                                                                                          Score 113.4; DB 12;
Pred. No. 8.2e-24;
                                                                                                                                                                                                                                                               113.4; DB 12;
No. 8.2e-24;
                                                                                                                                                                                                                                                                                                                     Score 113.4; DB 12;
Pred. No. 8.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 113.4; DB 12;
Pred. No. 8.2e-24;
                                                                                                                                                                                                                                                                                                                                                                          Score 113.4; DB 12;
Pred. No. 8.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.1%; Score 113.2; DB 4; 79.3%; Pred. No. 1.7e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                   Score 113.4; DB 6;
Pred. No. 8.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.1%; Score 113.2; DB 2; 73.8%; Pred. No. 6.3e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.1%; Score 113.2; DB 2
73.8%; Pred. No. 6.3e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.1%; Score 113.2; DB 6 76.0%; Pred. No. 9.5e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-DEC-2001.
(BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABA96879 standard; cDNA; 2522 BP.
Retinal binding site 12-encoding cDNA.
                                                                                                                                                                                                                                                                 Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ00870 standard; DNA; 56516 BP. PG1 genomic coding sequence. WO9932644-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ01022 standard; DNA; 56520 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA02618 standard; DNA; 78313 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADB72356 standard; DNA; 78313 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wild type PG1 coding sequence. WO9932644-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                              6.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                        6.2%;
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77.2%;
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77.2%;
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(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2003.
(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
RESULT 576
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                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                Query.Match
Best Local Similarity
RESULT 573
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Best Local Similarity
RESULT 574
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Best Local Similarity
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WO2003008583-A2.
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(GEST ) GENSET.
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                            RESULT 567
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                                                                                                                        Best
                                                                                                                                                                                                                                                                                                                                  AAK78096 standard; DNA; 1498 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAK81910 standard; DNA; 12466 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36722.
WO200157182-A2.
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                                                                                                                                                                                      ABL97459 standard; DNA; 7633 BP.
Human testicular antigen encoding DNA fragment SEQ ID NO: 2111.
WQ200155317-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 6.2%; Score 114.2; DB 4; Length 12466; Local Similarity 74.1%; Pred. No. 1.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 100944;
                                         AALO4536 standard; DNA; 7633 BP.
Human reproductive system related antigen DNA SEQ ID NO: 7224.
WO200155320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1498
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Human chromosome 2p21-22 fragment containing the DRIP gene.
WO2003093310-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA198065 standard; cDNA; 3591 BP.
Human neuroblastoma expressed polynucleotide SEQ ID NO 8.
WO200166733-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADQ59368 standard; DNA; 100944 BP.
Human cancer-associated (CA) gene sequence SEQ ID NO:4.
WO2004058288-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aυγυ/266 standard; DNA; 355211 BP.
Human cancer associated sequence HD08-023, SEQ ID 242.
WO20049060304-A2.
Loudtive system related antigen DNA SE.

PD 02-ANG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match
Best Local Similarity 80.5%; Pred. No. 4.9e-25;

ID MABD3459 standard; DNA; 7633 BP.

DE Human testicular antigen ence.

PD 02-ANG-200.
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                                                                                                                                                                                                                                                                                                                                                                                                                              6.2%; Score 114.4; DB 4;
81.8%; Pred. No. 2.8e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
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13-SEP-2001.
(CHIB-) CHIBA PREFECTURE.
(HISM ) HISAMITSU PHARM CO LTD.
(HISM ) HISAMITSU PHARM CO LTD.
6.2%; Score 114.4; DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 114; DB 2;
Pred. No. 7.9e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.2%; Score 114; DB 12; 75.9%; Pred. No. 5e-24;
                                                                                                                                                                                                                                 WOZOWIEL

02-AUG-2001.

(HUMAL) HUMAN GENOME SCI INC.

6.2%; Score 115; DB 4;

6.2%; Score 115; DB 4;

6.2%; Pred. No. 4.9e-25;
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Query Match
6.2%; Score 113.6; DB 1;
Best Local Similarity 74.8%; Pred. No. 7.1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX56595 standard; DNA; 114 BP.
Human 816576 DNA fragment.
WO9914241-A2.
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100.0%;
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(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-2004.
(SAGR-) SAGRES DISCOVERY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-1999.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-NOV-2003.
(UYBR-) UNIV BREMEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
RESULT 565
                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 560
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RESULT 564
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RESULT 561
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09-AUG-2001

Query Match

Query Match

Query Match

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RESULT

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Query Match

Query Match

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03-JUL-2003.
(INCY-) INCYTE GENOMICS INC.
(ery Match 6.1%; Score 112.6; DB 10; Length 214520;
ery Match 80.6%; Pred. No. 2.2e-23;
                                                                                                                                                                                                                                                      Length 155937;
                                                                                               DB 10; Length 78313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vuery Match 6.1%; Score 112.6; DB 6; Length 62944;
Best Local Similarity 78.9%; Pred. No. 1.1e-23;
RESULT 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Length 62944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A198077 standard; cDNA, 2267 BP.
Human neuroblastoma expressed polynucleotide SEQ ID NO 20.
Human neuroblastoma expressed polynucleotide SEQ ID NO 20.
HOSO166733-A1.
13-SEP-2001.
(CHIB-) CHIBA PREFECTURE.
(HISA) HISAMITSU PHARM CO LTD.
6.18; Score 112.6; DB 4; Length 2267;
st Local Similarity 77.4%; Pred. No. 1.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human reproductive system related antigen DNA SEQ ID NO: 5533. WO200155320-A2.
                                                                                                                                                                                                                                                                                                                                Human reproductive system related antigen DNA SEQ ID NO: 5534 WO200155320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 6670;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA197922 standard; cDNA; 2267 BP.
Human neuroblastoma expressed polynucleotide SEQ ID NO 3997.
WQ200166719-A1.
                                                                                                                                                     ADQ19389 standard; DNA; 155937 BP.
Human soft tissue sarcoma-upregulated DNA - SEQ ID 2208
WO2004048938-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL68262 standard; DNA; 62944 BP.
Kidney cancer related gene sequence SEQ ID NO:6599
WO200194629-A2.
                                                                                                                                                                                                                  PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
6.1%; Score 113.2; DB 12;
Best Local Similarity 79.3%; Pred. No. 1.2e-23;
RESULT 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G2-Aug-2001.
(HUMA-) HUMAN GENOME SCI INC.
6ry Match
6ry Match
76.6%; Pred. No. 2.5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL66947 standard; DNA; 62944 BP.
Lung cancer related gene sequence SEQ ID NO:5284
WO200194629-A2.
                                                                                                                                                                                                                                                                                                                                                       WOACCEDON.

02-AUG-2001.

(HUMAL) HUMAN GENOME SCI INC.

(HIMAL) GENOME SCI INC.

6.1%; Score 112.8; DB 4;

ery Match

76.6%; Pred. No. 2.3e-24;
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13-SEP-2001.
(CHIB-) CHIBA PREFECTURE.
(HISM ) HISAMITSU PHARM CO LTD.
HELY MATCh ---1arity 77.4%; Pred. No. 1.4e-24;
                                                                       (GAGR-) SAGRES DISCOVERY.

ry Match
6.1%; Score 113.2; DB 10
t Local Similarity 79.3%; Pred. No. 7.7e-24;
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ADE95866 standard; DNA; 78313 BP.
Human FYN gene genomic DNA sequence.
WO2003039484-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADL13471 standard; DNA; 214520 BP
                                                                                                                                                                                                                                                                                                            AAL02846 standard; DNA; 6670 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAL02845 standard; DNA; 7713 BP
                       ...d4-A2.
...dR-) SAGRES DISCO
...ery Match
Best Local Similarity 7.
RESULT 582
ID AD019389 stand>
DE Human soft
PD 10-7
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2001.
AL-) AVALON PHARN.
STY MATCH
BEST LOCAL SIMILATITY 7.
RESULT 589
ID ADULI 471 standa-
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PN WO20030"
PD 03-
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.SM | HISAMITSU E.

.fy Match

dest Local Similarity ',
RESULT 586

ID AA198077 standar'

DE Human neurob'
PN WO20016677

PD 13-SFF

PA (C''
PA
                                                                                                                                                                                                                                                                                                                                     July 2001.

July J. HUMAN GENOM.

July Match

Best Local Similarity

RESULT 584

ID AAL02845 stand?

DB Human reprrime PN W02001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-DEC-2001.
(AVAL-) AVALON PHARM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Rest Local Similarity
RESULT 585
ID AA197922 standard; cD
DE Human neuroblastoma e
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECT
PA (HISM ) HISAMITSU PHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-DEC-2001.
(AVAL-) AVALON PHARM.
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Best Local Similarity
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Best Local Similarity
RESULT 587
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AAK82548 standard; DNA; 1118 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37360.
W0200157182-A2.
(99-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 6.1%; Score 112.4; DB 10; Length 177531; Local Similarity 74.2%; Pred. No. 2.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.1%; Score 112.4; DB 10; Length 177531; 74.2%; Pred. No. 2.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 177531;
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1 (SUUD-) ST JUDE CHILDREN'S RES HOSPITAL.

QUERY MAICH 6.1%; Score 112.4; DB 10; Length 177531;

Best Local Similarity 74.2%; Pred. No. 2.3e-23;
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Best Local Similarity 74.2%; Pred. No. 2.3e-23;
                                                                                                                                                  Length 29328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1053;
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RESULT 590

ID ADR/7086 standard; DNA; 29328 BP.

ID Human cancer associated gene genomic sequence SEQ ID NO:132.

BN WO2004074321-A2.

PD 02-SEP-2004:

PA (SAGR-) SAGRES DISCOVERY INC.
                                                                                                                                                                                                                      ACF62732 standard; DNA; 177531 BP.
Cancer based on CYP3A5 related polymucleotide SEQ ID NO:660.
WO2003013534-A2.
20-FEB-2003.
(RPID-) EPIDAUROS BIOTECHNOLOGIE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                    ADB20847 standard; DNA; 177531 BP.
MRP1 based cancer related nucleic acid SEQ ID NO:660.
WO2003013533-A2.
                                                                                                                                     vuery Match 6.1%; Score 112.4; DB 13; Best Local Similarity 78.3%; Pred. No. 7.7e-24; RESULT 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.1%; Score 112.2; DB 2; Best Local Similarity 79.1%; Pred. No. 1.2e-24; RESULT 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.1%; Score 112.4; DB 8; 74.2%; Pred. No. 2.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 6.1%; Score 112.4; DB 1
Local Similarity 74.2%; Pred. No. 2.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB92110 standard; DNA; 177531 BP.
Human MDR1 related DNA sequence SEQ ID NO:660.
WO2003013535-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADH74617 standard; DNA; 177531 BP.
Human BAC clone GS1-259H13 CYP3AS genomic DNA.
US2003143537-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human MDR1 related DNA sequence SEQ ID NO:660.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADB87936 standard; DNA; 177531 BP.
Human UGT1A1 gene sequence SEQ ID NO:660.
20-FEB-2003.
(EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
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20-FEB-2003.
(EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA; 177531 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX30165 standard; DNA; 1053 BP.
Human secreted protein gene 21.
WO9910363-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAR-1999.
(HUMA-) HUMAN GENOME SCI INC.
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Best Local Similarity
RESULT 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADB96919 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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RESULT 596
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RESULT 611
                  Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37359
WO200157182-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACNO0803 standard; DNA; 1446 BP.

Breast cancer related marker, seq id 11953.
US200309974-Al.
29-MAY-2003.
(MILL-) MILLENNIUM PHARM INC.
ery Match
6.1%; Score 111.8; DB 11; Length 1446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 1815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
cy Match 6.1%; Score 112.2; DB 4; Length 5281;
t Local Similarity 72.4%; Pred. No. 3.1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 548;
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 8; Length 1815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.1%; Score 112.2; DB 8; Length 1815; 97.4%; Pred. No. 1.6e-24;
                                                                                                                                                                                                                                                          Length 1815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AALO4261 standard; DNA; 5281 BP.
Human reproductive system related antigen DNA SEQ ID NO: 6949.
WO200155320-A2.
                                                                                                 4; Length 1119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACC50499 standard; cDNA; 1815 BP.
Human secreted protein coding sequence, SEQ ID 166.
WQ200295010-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

ery Match

6.1%; Score 112.2; DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.1%; Score 111.8; DB 12; 98.3%; Pred. No. 1.1e-24;
                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
ry Match
t Local Similarity 97.4%; Pred. No. 1.6e-24;
                                             09-AUG-2010.
(HUMA-) HUMAN GENOME SCI INC.
(FUMA-) HUMAN GENOME SCI INC.
6.1%; Score 112.2; DB 4
ery Match 77.7%; Pred. No. 1.2e-24;
                                                                                                                                                                                                                                                                                                                                                                      27-DEC-2002.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
6-14; Score 112.2; DB 8
6-17 Match
6-17 Match
7-1 G'milarity 97.44; Pred. No. 1.6e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.1%; Score 112.2; DB 1097.4%; Pred. No. 1.6e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACH80161 standard; DNA; 548 BP.
Human genome derived single exon probe #13356.
US2003194704-Al.
                                                                                                                                      Human secreted protein gene 26 SEQ ID NO:36. W0200017222-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADA56101 standard; DNA; 1815 BP.
Gene encoding human secreted protein #280.
WO2002102994-A2.
                                                                                                                                                                                                                                                                                                                ADA39913 standard; cDNA; 1815 BP.
Human secreted protein encoding cDNA.
WO2002102993-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC87234 standard; DNA; 21581 BP. Human GPCR gene SEQ ID NO:1687. EP1270724-A2.
AAK82547 standard; DNA; 1119 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
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Best Local Similarity
RESULT 607
                                                                                                         Best Local Similarity RESULT 600
                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 601
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
RESULT 604
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PA PER PA
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ABK43076 standard; DNA; 32169 BP.
Genomic sequence #975 encoding novel human connective tissue polypeptide.
WO200155343-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADRO6591 standard; cDNA; 4865 BP. Full length human cDNA useful for treating neurological disease Seq 97. EP1447413-A2.
                                                                                                                                                                                                                                                                                                                                                                  Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 111.8; DB 11; Length 118931; Pred. No. 2.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMAN GENOME SCI INC.
ry Match
t Local Similarity 76.5%; Pred. No. 1.4e-23;
                                                                                                 02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
PRY MATCH
st Local Similarity 76.5%; Pred. No. 1.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.0%; Score 111.4; DB 13; Length 4865; 79.8%; Pred. No. 5.4e-24;
                                                                                                                                                                                                                                                                                                    Length 32169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA differentially expressed in granulocytic cells #147.
WO200228999-A2.
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                                                                                                                                                                                                                                                                                                    6.1%; Score 111.8; DB 9; 76.5%; Pred. No. 1.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 6.0%; Score 111.4; DB 2; Local Similarity 58.1%; Pred. No. 8.6e-25;
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11-APR-3002.
(GENE J. GENE LOGIC INC.
6.0%; Score 111.4; DB 6;
ATV MATCH 6.0%; Pred. No. 3.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.0%; Score 111; DB 4;
80.1%; Pred. No. 2.5e-24;
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(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
(ery Match 6.0%; Score 111; DB 5;
  76.5%; Pred. No. 1.9e-24;
                                                                                                                                                                                                ADB61232 standard; DNA; 32169 BP.
Connective tissue related genomic DNA #975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human channel/transporter gene #21
WO200154472-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human polynucleotide SEQ ID NO 8711. WQ200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACN44586 standard; DNA; 118931 BP. Human genomic sequence hCG30014. WO2003073826-A2.
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(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                            AAK86139 standard; DNA; 37736 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 6.1%;
Local Similarity 75.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX56597 standard; DNA; 242
Human 951273 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
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(GETH ) GENENTECH INC.
Best Local Similarity
RESULT 608
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RESULT 610
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RESULT 615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-SEP-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                        US2003054375-A1.
                                                                                                                                                                                                                                                              20-MAR-2003
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(SOPP/) SOPPET D R. (GENT/) GENTZ R L. (WEIY/) WEI Y. (MOOR/) MOORE P A. (YOUN/) YOUNG P B. (GREE/) FERRIB J M.. (FERR/) FERRIB A M..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003004622-A2.
16-JAN-2003.
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(RUBE/) I
(LIYY/) I
(ZENG/) I
(KYAW/) I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD44878 standard, cDNA, 1022 BP.
Human secreted protein-encoding gene 25 cDNA clone HTEBB42, SEQ ID NO:35.
US2002076756-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein-encoding gene 25 cDNA clone HTEEB42, SEQ ID NO:35.
US2002077287-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP56686 standard; cDNA; 972 BP.
Human junction adhesion molecule 2 splice variant (huJAM2sv) cDNA,
WO2004053058-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Luidix & CO ELI.

Best Local Similarity 54.0%; Score 111; DB 12; Length 972; RESULT 621

ID AAV34310 standard; DNA; 1022 BP.
DE Human secreted protein gene 25.7.
PD 17-SEP-1999

PA (FILL 1999)
                                                        E Human junctional adhesion molecule 2 (huJAM2) coding sequence. PN WC2003008541-A2.
PD 30-JAM-2003.
PA (ELLL) LILLY & CO ELI.
Query Match
Best Local Similarity 54.0%; Score 111; DB 8; Length 897;
Best Local Similarity 54.0%; Pred. No. 2.6e-24;
ID AAF74414 standard; DNA; 905 BP.
DE Angiogenesis protein AAA1 nucleotide sequence (Fig 7).
PN WC200110186-A2.
PD 15-FEB-2001.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 930;
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PN WOZOON11086-A2.
PD 15-FEB-2001
PA (EOSB-) EOS BIOTECHNOLOGY INC.
QUELY MATCh
Best Local Similarity 54.0%; Pred. No. 2.6e-24;
RESULT 619
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ry Match 6.0%; Score 111; DB 2;

t Local Similarity 54.0%; Pred. No. 2.8e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.0%; Score 111; DB 6; 54.0%; Pred. No. 2.8e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAI61103 standard; cDNA; 930 BP.
Human polynucleotide SEQ ID NO 5092.
WO200153312-A1.
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                                         AAL51599 standard; DNA; 897 BP.
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JR/)
JR/)
JR//
GREE/
GREE/
GREER,
FERRIE A

LETY MATCH

JSULT 623
LD AAD44878 standard;
DE Human secreted pr
PD 20-JUN-2002.
PA (RUBE/) RUB
PA (RUBE/) RC
PA (ROSE/) 
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RESULT 622

RESULT 622

DE ANDA 622

E Human secreted proteil
PN US2002077287-A1.
PA (RUBE)
PA (RUBE)
PA (RUBE)
PA (RUBE)
PA (RUBE)
PA (LIYY)
LI Y.
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LI H.
PA (ROPP)
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ZENG Z.
KYAW H.
FISCHER C L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
RESULT 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUL-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
       RESULT 617
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..; 1022 BP.
..i. 1024 BP.
..i. 1024 BP.
..i. 1024 BP.
..i. 1025 BP.
..i. 1025 BP.
..i. 1026 BP.
..i. 1027 BP.
..i. 1022 BP.
..i. 1032 BP.
..i
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E Human secreted protein-related DNA - SEQ ID 349.

N W02003038063-A2.

N 08-MAY-2003.

A (HUMA-) HUMAN GENOME SCI INC.

Query Match

Est Local Similarity 54.0%; Pred. No. 2.8e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.0%; Score 111; DB 8; Length 1022; 54.0%; Pred. No. 2.8e-24;
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Query Match
6.0%; Score 111; DB 9; Length 1022;
Best Local Similarity 54.0%; Pred. No. 2.8e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cDNA from secreted protein gene 25. US2003225009-A1.
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Human secreted protein cDNA #SEQ ID 232.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LI Y.
ZENG Z.
KYAW H.
FISCHER C L.
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RESULT 629
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RESULT 628
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RUBEN S M.
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RESULT 639
                                                                                                                                                         Length 1022;
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                                                                                                                                                                                                                                                                                              6.0%; Score 111; DB 2; Length 1076; 54.0%; Pred. No. 2.9e-24;
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                                                                                                                                                                                               AAV82780 standard; cDNA; 1076 BP.
Clone ct684 4 isolated from human adult brain cDNA library
WO9842739-AZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACS8S86 standard; cDNA; 1295 BP.
Human PRO245 protein UNQ219 encoding cDNA SEQ ID NO:35.
WO200053758-A2.
14-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX81770 standard; cDNA; 1295 BP.
cDNA DNA35638 encoding A33 related antigen PRO245.
WO9927098-A2.
                                                                                                                                                       Query Match 6.0%; Score 111; DB 12;
Best Local Similarity 54.0%; Pred. No. 2.8e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.0%; Score 111; DB 6; 54.0%; Pred. No. 2.9e-24;
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Human junctional adhesion protein (JAM2) cDNA.
WO200114404-A1.
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Protein PRO245 cDNA clone DNA35638-1141.
WO9914328-A2.
                                                                                                                                                                                                                                                                                                                                  Human polynucleotide SEQ ID NO 14. US2002065334-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001.
(TEXA-) TEXAS BIOTECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX37664 standard; cDNA; 1295 BP.
Human PRO245 cDNA.
WO9914241-A2.
                                                                                                                                                                                                                                                            (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                  (JACO/) JACOBS K.
(MCCO/) MCCOY J M.
(LAVA/) LAVALLIE E R.
(COLL/) COLLINS-RACIE I.
(EVAN/) EVANS C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUN-1999.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-1999.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MERB/) MERBERG D.
(TREA/) TREACY M.
(SPAU/) SPAULDING V.
                                                                                                                                         HASTINGS G A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity RESULT 632
                                                                (MOOR/) MOORE P A.
(YOUN/) YOUNG P E.
(GREE/) GREENE J M.
(FERR/) FERRIE A M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
RESULT 634
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Best Local Similarity
RESULT 633
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                                  GENTZ R L.
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PA
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AAC97437 standard, cDNA, 1295 BP.
Human anglogenesis-associated protein PRO245 cDNA, SEQ ID NO:90.
WO200053753-A2.
                                                                                               PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 638
                                                                                                                                                                                                                                                                                                              Length 1295;
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Human cDNA clone DNA35638-1141 encoding PRO245 (UNQ219)
WO200119991-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAGOS2 standard; cDNA; 1295 BP.
Human cDNA for secreted/transmembrane protein PRO245.
US2003003530-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA sequence encoding for PRO245 polypeptide WO200140466-A2.
                                                                                                                                                                                                                                                                         08-JUN-2000.
(GETH ) GENENTECH INC.
6.0%; Score 111; DB 3;
rry Match 6.0%; Pred. No. 3.2e-24;
Best Local Similarity 54.0%; Pred. No. 3.2e-24; RESULT 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 6.0%; Score 111; DB 3;
Local Similarity 54.0%; Pred. No. 3.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vuery Match 6.0%; Score 111; DB 4;
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 642
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Local Similarity 54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 645
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54.0%; Pred. No. 3.2e-24;
                                                 AAZ52202 standard; cDNA; 1295 BP.
Human PRO245 protein encoding cDNA, UNQ219.
WO200015797-A2.
                                                                                                                                                                                                      AAA77562 standard; cDNA; 1295 BP.
Human PRO245 cDNA sequence SEQ ID NO:66.
WO200032221-A2.
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Human PRO245 cDNA.
WO200073452-A2.
                                                                                                                                                                                                                                                                                                                                                                      ADC78383 standard; cDNA; 1295 BP.
Human PRO245 cDNA.
WO200015796-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF72383 standard; cDNA; 1295 BP.
Human PRO245 cDNA.
WO200104311-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 644
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Best Local S
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ABX89308 standard; cDNA; 1295 BP.

DNA encoding novel secreted and transmembrane protein PRO245.
US2003017563-A1.
23-JAN-2003.

(GETH ) GENENTECH INC.
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            ACD07452 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2002197671-A1.
26-DEC-2002.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                   ABX71500 standard; cDNA; 1295 BP.
Human cDNA encoding secreted/transmembrane protein PRO245.
US2002132240-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 654

ID ACD20057 standard; CDNA; 1295 BP.

DE Human secreted / transmembrane polypeptide PRO245 CDNA.

PN US2003036606.A1.

PD 20-FEB-2003.

PA (GETH ) GENENTECH INC.

f n%: Score 111; DB 8; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACD41962 standard; cDNA; 1295 BP.

Human secreted/transmembrane protein (PRO) cDNA #168.
US2003036179-A1.
CO-FEB-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                            ACHOG6812 standard; cDNA; 1295 BP.
Human secreted/transmembrane polypeptide PRO245 cDNA.
US2003044839-Al.
                                                                                                   Query Match
Best Local Similarity 54.0%; Score 111; DB 8;
RESULT 647.0%; Pred. No. 3.2e-24;
RESULT 647.00 Standard; CDNA; 1295 BP.
DE CDNA encoding human PRO polypeptide #168.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
(ery Match
(ery Match 7.0 milarity 54.0%; Pred. No. 3.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 650
DE ABX9308 standard; CDNA, 1295 BP.
DE DNA encoding novel secreted and transmembrane pip N32003017563-A1.
PP 23-JAN-2003.
PP GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 111; DB 8;
Pred. No. 3.2e-24;
                                                                                                                                                                                                                                                   6.0%; Score 111; DB 8; 54.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACA05390 standard; cDNA; 1295 BP.
cDNA encoding human secreted protein PRO245.
US2003023054-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABX96069 standard; cDNA; 1295 BP.
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54.0%;
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(GETH ) GENENTECH INC.
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2003.

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Z.Y MATCH

Best Local Similarity 5
RESULT 651

ID ACD41962 stander

DE Human secret

PN US2030-
PD 20-
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(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                            Best Local Similarity RESULT 648
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RESULT 652
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Best Local Similarity
RESULT 649
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RESULT 655
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                                                                                                                                                                                                                                                   Query Match
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RESULT 646
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Human cDNA encoding a secreted/transmembrane protein, SEQ ID 335. US2003032155-A1.
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N US2003092002-A1.

D 15-MAY-2003.

A (GETH ) GENENTECH INC.

6.0%; Score 111; DB 9; Length 1295;

Best Local Similarity 54.0%; Pred. No. 3.2e-24;
                                                                                                                                                                                     Length 1295;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted / transmembrane polypeptide PRO245 cDNA US200207143-A1.
06-FB3-2003 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAS4860 standard; CDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245
US2003017463-A1.
33-JAN-2003.
(GETH ) GENENTECH INC.
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ABX93348 standard; cDNA; 1295 BP.
cDNA encoding human A-33 related antigen PRO245.
US20022206-A1.
G5-DEC-2002.
(GETH ) GENENTECH INC.
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(GETH) GENENTECH INC.
(GETH) GENENTECH INC.
6.0%; Score 111; DB 9;
ery Match
54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 658
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                                                                                                                                                                              Score 111; DB 8;
Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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                                                                                                                                                                              6.0%;
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54.0%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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L2003.

LETH ) GENENTECH LOCAL SMILLARING SERVICH GOTO SMILL SM
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Best Local Similarity
RESULT 660
                                                                                                                                                                                                           Best Local Similarity
RESULT 656
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                                                                                                                                                                                                                                                                                         ACA04191 standard;
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US2003049816-A1.
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Length 1295;

Length 1295;

Length 1295;

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ADAB/1466 standard; CDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 CDNA.
2820030845-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003073211-A1.
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                                                                                                                                                                                                                                                                                                  Query Match
Beet Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 675
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 678
                                                                                   6.0%; Score 111; DB 9; 54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 680
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54.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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                                                                                                                                                              Human PRO polynucleotide #168.
US2003082705-A1.
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Human PRO polynucleotide #11.
US2003044793-A1.
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Human PRO polynucleotide #168.
US2003082763-A1.
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Human PRO polynucleotide #168.
US2003087351-A1.
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01-MAY-2003.
(GETH ) GENENTECH INC.
4.0%; SC
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US2003087349-A1.
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Local Similarity 54.0%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                           GENENTECH INC.
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(GETH) GENENTECH INC.
                                                                                      Query Match
Best Local Similarity
RESULT 674
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RESULT 676
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     US2003082693-A1.
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(GETH ) GEN
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Novel human secreted and transmembrane protein PRO245 cDNA.
122003069796-A1.
10-ARR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                    ADA86363 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA, 22003082111-Al.
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Novel human secreted and transmembrane protein PRO245 cDNA.
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US2003045693-A1.
                                                                                                                                                                                                                                                                                                                                         Query Match 6.0%; Score 111; DB 9;
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 666
                                                                                                                 6.0%; Score 111; DB 9;
54.0%; Pred. No. 3.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.0%; Score 111; DB 9; Best Local Similarity 54.0%; Pred. No. 3.2e-24; RESULT 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.0%; Score 111; DB 9; 54.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADA18124 standard; cDNA; 1295 BP.
Human secreted/transmembrane protein cDNA, #13.
US2003039971-A1.
27-FBB-2003.
                                                                                                                                                                                               ADB27884 standard; cDNA; 1295 BP.
CDNA encoding human PRO polypeptide #168.
US2003082704-A1.
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CDNA encoding human PRO polypeptide #168.
US2003068794-A1.
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Human PRO polynucleotide #168.
US2003087350-A1.
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Human PRO polynucleotide #168.
US2003073215-A1.
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Human PRO polynucleotide #168.
US2003068795-A1.
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                                                                                                                                                                                                                                                                                   01-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 668
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Best Local Similarity
RESULT 672
                                                                                                                                   Best Local Similarity RESULT 665
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                                                                                                                    Ouery Match
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Length 1295;

Length 1295;

Length 1295;

Length 1295;

Length 1295;

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RESULT 673

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Length 1295;

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(GETH ) GENENTECH INC.
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6.0%; Score 111; DB 9; Length 1295;
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 691
                                 Length 1295;
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                                                                                                                                                                                                                          ADB19895 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2003082691-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003044945-Al.
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Best Local Similarity 54.0%; Score 111; DB 9;
RESULT 687

DE ADA/461 standard; CDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PD 10-APR-2003.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                  6.0%; Score 111; DB 9; 54.0%; Pred. No. 3.2e-24;
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                               Ouery Match 6.0%; Score 111; DB 9;
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 683
                                                                                                                                                                         6.0%; Score 111; DB 9; 54.0%; Pred. No. 3.2e-24;
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54.0%; Pred. No. 3.2e-24;
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Human PRO polynucleotide SEQ ID NO 335.
US2003077713-A1.
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US2003082701-A1.
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                                                                              ADA93999 standard; cDNA; 1295 BP.
Human PRO polynucleotide #168.
US2003077722-A1.
24-APR-2003.
(GETH ) GENENTECH INC.
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Human PRO polynucleotide #168.
US2003082710-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
17-APR-2003.
(GETH ) GENENTECH INC.
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2ry Match
Best Local Similarity best Local Similarity best Local Similarity best Human PRO representation by US20030.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 690
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vuery Match
Best Local Similarity 54.0%; Score 111; DB 9; Length 1295;
RESULT 697
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Length 1295;
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                                             ADA85259 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2003082695-A1.
                                                                                                                                                                  AUA84707 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2003082708-Al.
                                                                                  PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 693
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 699
6.0%; Score 111; DB 9; 54.0%; Pred. No. 3.2e-24;
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54.0%; Pred. No. 3.2e-24;
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Human PRO polynucleotide SEQ ID NO 335.
US2003077715-A1.
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US2003082761-Al.
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US2003073210-A1.
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Human PRO polynucleotide #11.
US2003064367-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Query Match
Best Local Similarity
RESULT 692
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Best Local Similarity 54.0%; Pred. No. 3.2e-24; RESULT 710

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O1-MAY-2003.
(GETH ) GENENTECH INC.
6.0%; Score 111; DB 9; Length 1295;
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003082765-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.0%; Score 111; DB 9;
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 705
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 708
                                                           6.0%; Score 111; DB 9; 54.0%; Pred. No. 3.2e-24;
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54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 709
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cDNA encoding human PRO polypeptide #168.
US2003096386-A1.
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cDNA encoding human PRO polypeptide #168.
US2003082760-A1.
                                                                                                               ADB26780 standard; cDNA; 1295 BP.
cDNA encoding human PRO polypeptide #168.
US2003092147-A1.
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Human PRO polynucleotide SEQ ID NO 335.
US2003077714-A1.
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Human PRO polynucleotide #168.
US2003082690-A1.
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Human PRO polynucleotide #168.
US2003082759-A1.
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US2003082702-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
Loy Match
Best Local Similarity
RESULT 701
ID ADB26780 stand>
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PN US20030*
PD 15-
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Best Local Similarity
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RESULT 702
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US2003049817-A1.
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(GETH ) GEN
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Query Match 6.0%; Score 111; DB 9; Length 1295; Best Local Similarity 54.0%; Pred. No. 3.2e-24; RESULT 711
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                                                                                                                                                                                                                                                                                                                  ADA86915 standard, cDNA, 1295 BP.
Novel human secreted and transmembrane protein PRO245 CDNA.
US2003082709-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADABSO18 standard; CDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 CDNA.
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 715
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54.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUA16523 standard; CDNA; 1295 BP.
Human secreted/transmembrane protein CDNA, #13
US203333959-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted/transmembrane protein cDNA, #13
                                                                                                                                                                            cDNA encoding human PRO polypeptide #168.
US2003077710-A1.
ADA77492 standard; cDNA; 1295 BP. Human PRO polynucleotide #168. US2003068797-A1.
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(GETH ) GENENTECH INC.
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01-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 716
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Query Match
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003087344-Al.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003073213-A1.
                                                                                                                 Query Match
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 720
DE ADBASH36 standard; CDNA, 1295 BP.
DE CDNA encoding human PRO polypeptide #168.
PD 01-MAY-2003.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 54.0%; Score 111; DB 9;
RESULT 724

DE ADA97575 standard; CDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PP 01-MAY-2003.
PP 01-MAY-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 721
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 722
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54.0%; Pred. No. 3.2e-24;
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RESULT 719

ID ADA42670 standard; CDNA; 1295 BP.

DE Human secreted/transmembrane protein CDNA, #13.

PN US2003054351-A1.

PD 20-MAR-2003.

FO COMMAR-2003.

FOR CGETH ) GENENTECH INC.
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US2003082706-A1.
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US2003022239-A1.
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Human PRO polynucleotide #168.
US2003059909-A1.
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Human PRO polynucleotide #11.
US2003064923-A1.
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Human PRO polynucleotide #168.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Beet Local Similarity
RESULT 726
ID ADB22265 standard; cl
DE Novel human secreted
PN US2003087344-A1.
PD 08-MXY-2003.
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Best Local Similarity
RESULT 728
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RESULT 727
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wery Match
Best Local Similarity 54.0%; Score 111; DB 10; Length 1295;
RESULT 736
ID ADB89627 standard; CDNA, 1295 BP.
Br Human PRO polynucleotide #168
PN US2003082698-A1.
PN US2003082698-A1.
uery Match
6.0%; Score 111; DB 9; Length 1295;
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 729
1D ADB22817 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168
PN US2003077711-A1.
PD 24-APR-2007
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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Novel human secreted and transmembrane protein PRO245 cDNA.
US200308276-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO245 cDNA,
US2003082712-A1.
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 731
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 734
                                                                                                                                                                                                                                                                                                                                                             ADB23590 standard; cDNA; 1295 BP.
Human PRO polynucleotide SEQ ID NO 335.
US2003077712-A1.
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ID ADB15375 standard; cDNA; 1295 BP.
DE Human PRO polymucleotide #168.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
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Human PRO polynucleotide #168.
US2003082762-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 730
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Length 1295;

Length 1295;

Length 1295;

RESULT 738

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/ Match 6.0%; Score 111; DB 10; Length 1295; Local Similarity 54.0%; Pred. No. 3.2e-24;
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Novel human secreted and transmembrane protein PRO245 CDNA.
US2003082692-Al.
                     Score 111; DB 10;
Pred. No. 3,2e-24;
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Pred. No. 3.2e-24;
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Best Local Similarity' 54.0%; Pred. No. 3.2e-24;
RESULT 750
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Human secreted/transmembrane protein cDNA, #13
US2003036061-Al.
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US20030494576-A1.
USAR-2003.
(GETH ) GENENTECH INC.
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US2003059772-A1.
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US2003059829-A1.
                                                                         ADB35004 standard; cDNA; 1295 BP.
Human PRO polynucleotide SEQ ID NO 335.
US2003077718-Al.
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Human PRO polynucleotide SEQ ID NO 335.
US2003077720-A1.
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                   6.0%;
54.0%;
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RESULT 748
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54.0%;
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Local Similarity 54.0%;
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(GETH ) GENENTECH INC.
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                                 Best Local Similarity RESULT 747
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RESULT 753
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Best Local Similarity
RESULT 752
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                       Query Match
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                                       Length 1295;
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                                                                                                                                                                                                                              Aubsy460 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB47083 standard; CDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 CDNA.
US2003082687-Al.
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Novel human secreted and transmembrane protein PRO245 CDNA,
03.0020082696-Al.
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 743
                                                                                                                                                                                                                                                                                                                                             6.0%; Score 111; DB 10; 54.0%; Pred. No. 3.2e-24;
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                                 Query Match 6.0%; Score 111; DB 10;
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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54.0%; Pred. No. 3.2e-24;
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                                                                                                           Human secreted/transmembrane protein cDNA, #13 US2003077654-A1.
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Human PRO polynucleotide SEQ ID NO 335.
US2003077717-Al.
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Human PRO polynucleotide SEQ ID NO 335.
US2003077716-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADB86690 standard; cDNA; 1295 BP.
Human PRO polynucleotide #168.
US2003082697-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                       ADB74725 standard; cDNA; 1295 BP
                                                                                           ADB77589 standard; cDNA; 1295
01-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 742
                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 739
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RESULT

3 5 5 5 E

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A B B B B

Length 1295;

Length 1295;

Length 1295;

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Length 1295;

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Best Local Similarity 54.0%; Pred. No. 3.2e-24; RESULT 765
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Novel human secreted and transmembrane protein cDNA Seq ID335.
US2003087365-A1.
                                 6.0%; Score 111; DB 10; Length 1295; 54.0%; Pred. No. 3.2e-24;
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003092106-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003092105-Al.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003092107-A1.
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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Human secreted/transmembrane protein cDNA, #13.
US2003054400-A1.
(GETH ) GENENTECH INC.
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Human secreted/transmembrane protein cDNA, #13.
US2003054441-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC33785 standard; cDNA; 1295 BP.
Human secreted/transmembrane protein cDNA, #13.
US2003073077-A1.
                                                                                                     Human secreted/transmembrane protein cDNA, #13 US2003049677-A1.
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(GETH ) GENENTECH INC.
6.0%; Score 111;
                                                                                   ADC28795 standard; cDNA; 1295 BP.
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Best Local Similarity 54.0%; Pr
RESULT 758
ID ADC1937 standard; cDNA; 1295 FD
PN WISCOSSO441.A1.
PD 20-MAR-2003.
PAR-2003.
PAR-C1054 PAR-C107.
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54.0%;
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54.0%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 760
ID ADC12855 standard; cD
DE Human secreted/transm
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC
Query Match
Best Local Similarity
RESULT 756
ID Anchart
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Best Local Similarity
RESULT 757
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RESULT 759
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Best Local Similarity
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Best Local Similarity
RESULT 764
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ID ADC719
DE Novel
PN US2003
PD 15-MAY
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AUC5/263 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein cDNA Seq ID335.
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Novel human secreted and transmembrane protein cDNA Seq ID335.
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Novel human secreted and transmembrane protein cDNA Seg ID335.
US2003087363-A1.
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US2003087364-A1.
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Novel human secreted and transmembrane protein cDNA Seg ID335.
US2003087360-A1.
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                                                                                                         Score 111; DB 10; Length 1295;
Pred. No. 3.2e-24;
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                                                                                                                                           ADC60454 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PR0245 cDNA.
                                                                                                                                                                                                                                                                                                     ADCS0929 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2003087361-A1.
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 768
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Human PRO polynucleotide #168.
US2003087362-A1.
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08-MAY-2003.
(GETH ) GENENTECH INC.
March 6.0%; SC
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Best Local Similarity 54.0%;
RESULT 772
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(GETH ) GENENTECH INC.
                                                                   08-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 773
                                                                                                                          Local Similarity
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RESULT 769
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Best Local Similarity
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                                                                                                           Query Match
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RESULT 766
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ADC47908 standard; cDNA; 1295 BP.

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Ouery Match 6.0%; Score 111; DB 10; Length 1295;
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 782
                                                                                                                  Length 1295;
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                                                                                                                                                                        ADD03160 standard; cDNA; 1295 BP.

Novel human secreted and transmembrane protein PRO245 cDNA.
US2003093104-A1.
15-MAY-2003.
                                                                                                                                                                                                                                                                                                                                    ADC90152 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2003087348-A1.
08-MAY-2003.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003087354-Al.
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Novel human secreted and transmembrane protein PR0245 cDNA.
                  Leary Match

Best Local Similarity 54.0%; Score 111; DB 10; Lear RESULT 775

ID ADD03160 standard; cDNA; 1295 BP.

DE Novel human secreted and train PD 12.003092104-A1.

PD 12.MAY-2007
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 780
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Pred. No. 3.2e-24;
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                ADC12307 standard; cDNA; 1295 BP.
Human secreted/transmembrane protein cDNA, #13.
US2003082541-A1.
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cDNA encoding human PRO polypeptide #168.
US2003194770-A1.
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Human PRO polynucleotide #168.
US2003194773-A1.
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Human PRO polynucleotide #168.
US2003194776-A1.
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Human PRO polynucleotide #168.
US2003194774-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 783
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RESULT 774
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Length 1295;
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003087358-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA
US2003203438-A1.
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                                                                        6.0%; Score 111; DB 10; 54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Human secreted/transmembrane protein cDNA, #13.
US2003104381-A1.
                                                                                                                      ADD04862 standard; cDNa; 1295 BP.
Human secreted/transmembrane protein cDNA, #13.
US2003104469-A1.
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Human secreted/transmembrane protein cDNA, #13
US2003108983-A1.
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US2002194792-A1.
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US2003194769-A1.
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US2003194775-Al.
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05-JUN-2003.
(GETH ) GENENTECH INC.
6.0%; SC
Human PRO polynucleotide #168.
US2003194771-A1.
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Local Similarity 54.0%;
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Local Similarity 54.0%;
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(GETH ) GENENTECH INC.
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                                                                        Query Match
Best Local Similarity
RESULT 784
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RESULT 785
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RESULT 792
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US2003199056-A1.
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                                                                 6.0%; Score 111; DB 10; Length 1295; 54.0%; Pred. No. 3.2e-24;
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003203432-Al.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003194765-Al.
 Novel human secreted and transmembrane protein PRO245 cDNA.
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Best Local Similarity 54.0%; Score 111; DB 10;
RESULT 798
ENGLIC 798
ENGLIC 4D91365 standard; CDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PD 23-0CT-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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cDNA encoding human PRO polypeptide #168.
US2003194779-A1.
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cDNA encoding human PRO polypeptide #168.
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Human PRO polynucleotide #168.
US2003203431-A1.
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Human PRO polynucleotide #168.
US2003203430-A1.
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Human PRO polynucleotide #168.
US2003199030-A1.
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Best Local Similarity 1.

RESULT 793
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Best Local Similarity
RESULT 794
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RESULT 800
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RESULT 801
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vuery Match 6.0%; Score 111; DB 10; Length 1295;
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 808
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003194791-A1.
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PA (GETH ) GENENTECH INC.

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Best Local Similarity 54.0%; Pred. No. 3.2e-24;

RESULT 803
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Pred. No. 3.2e-24;
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54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 810
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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US2003207417-A1.
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Human PRO polynucleotide #168.
US2003199025-A1.
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Human PRO polynucleotide #168.
US2003194772-A1.
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Human PRO polynucleotide #168.
US2003199023-A1.
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Human PRO polynucleotide #168.
US2003199053-A1.
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                                                                                                 ADD79432 standard; cDNA; 1295 BP.
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Local Similarity 54.0%;
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Best Local Similarity 54.0%;
RESULT 807
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(GETH ) GENENTECH INC.
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RESULT 802
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RESULT 806
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(GETH ) GENENTECH INC.
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06-NOV-2003.
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                                      6.0%; Score 111; DB 10; Length 1295; 54.0%; Pred. No. 3.2e-24;
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Beet Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 813
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 814
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADE12828 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2003194766-A1.
                                                                                                                                                                                                Ouery Match
Best Local Similarity 54.0%; Score 111; DB 10;
RESULT 812
BLO ADE18889 standard; CDNA; 1295 BP.
DE Human PRO polynuclectide #168.
PP 23-0073-99026-A1.
PP 23-0072-2003.
PA (GETH ) GENENTECH INC.
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54.0%; Pred. No. 3.2e-24;
                                                                                               ADE34696 standard; cDNA; 1295 BP.
Human secreted/transmembrane protein cDNA, #13.
US200307583-A1.
(GETH ) GENENTECH INC.
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US2003207418-A1.
06-NOV-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADD78878 standard; cDNA; 1295 BP.
cDNA encoding human PRO polypeptide #168.
US2003203429-A1.
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cDNA encoding human PRO polypeptide #168.
US2003199064-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE43085 standard; cDNA; 1295 BP. Human PRO polynucleotide #168. 023003199033-A1. 03-0CT-2003. (GETH ) GENENTECH INC.
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Human PRO polynucleotide #168.
US2003199059-A1.
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Human PRO polynuclectide #168.
US2003199032-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                   Best Local Similarity RESULT 811
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Best Local Similarity
RESULT 815
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RESULT 819
23-OCT-2003
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                                      Query Match
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vuery Match 6.0%; Score 111; DB 10; Length 1295;
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 820
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Pred. No. 3.2e-24;
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Novel human secreted and transmembrane protein PRO245 cDNA
US2003207355-A1.
                                                                                                                                                                                                       Query Match 6.0%; Score 111; DB 10;
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 821
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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Human PRO polynucleotide #168.
US2003199031-Al.
                                                                                              ADD89564 standard; cDNA; 1295 BP.
Human PRO polynucleotide #168.
US2003199028-A1.
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Human PRO polynucleotide #168.
US2003199034-A1.
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Human PRO polynucleotide #168.
US2003207370-A1.
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Human PRO polynucleotide #168.
US2003194777-A1.
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Local Similarity 54.0%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 825
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Best Local Similarity 54.0%; Score 111; DB 10; Length 1295; RESULT 83.2 ID ADH55817 standard; CDNA, 1295 BP. BE Novel human secreted and transmip N US2003207379-A1. PD 06-NOV-2003
   6.0%; Score 111; DB 10; Length 1295; 54.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207379-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207385-Al.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207386-Al.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207387-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
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Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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Human secreted/transmembrane protein cDNA, #13.
US2003054352-A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                       Human secreted/transmembrane protein cDNA, #13.
US2003039972-A1.
                                                                     Human DNA35638 CDNA encoding PRO245 protein.
US2003171568-A1.
                                                        CDNA; 1295 BP
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54.0%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                     (ASHK/) ASHKENAZI A.
(FONG/) FONG S.
(GODD/) GODDARD A.
(GURA/) GURBER A L.
(NAPI/) NAPIER M A.
(TUMA/) TUMAS D.
(WOOD/) WOOD W I.
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
RESULT 811
ID ADH55265 standard; cD
DE Novel human secreted
PN US2003207381-A1.
PD 06-NOV-2003.
Query Match
Best Local Similarity
BESULT 829
ID ADH62535 standard; cD
DE Human DNA35638 cDNA e
PN US2003171568-A1.
PN (L-SEP-2003.
PA (RAHK/) ASHKENAZI A.
PA (GODD/) GODDARD A.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAM/) TUNAS D.
PA (TUNA/) TUNAS D.
PA (WOOD/) WOOD W I.
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Best Local Similarity
RESULT 837
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RESULT 830
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Length 1295;
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Local Similarity 54.0%; Pred. No. 3.2e-24;
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Novel human secreted and transmembrane protein PRO245 CDNA.
12-pren 2200302156-A1.
ADH81898 standard; cDNA; 1295 BP. Novel human secreted and transmembrane protein PRO245 cDNA. US2003207388-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207377-Al.
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Novel human secreted and transmembrane protein PRO245 cDNA
US2003087355-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003087353-A1.
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 840
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Query Match
Best Local Similarity 54.0%; Pred. No. 3.2e-24;

RESULT 844
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 842
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54.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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US2003054349-A1.
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cDNA encoding human PRO polypeptide #168.
02-JAN-2003.
(GETH ) GENENTECH INC.
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cDNA encoding human PRO polypeptide #11.
US2002192659-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACA58948 standard; cDNA; 1295 BP.
Human PRO polynucleotide #11.
US2002146709-A1.
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ID ADJ26226 standard; cDNA; 1295 BP.
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54.0%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 845
                                                                                                                                                                                                                        Local Similarity
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Best Local S:
RESULT 838
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13-NOV-2003.
(GETH ) GENENTECH INC.
      US2003211571-A1.
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Pred. No. 3.2e-24;
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                                                                                   Length 1295
Novel human secreted and transmembrane protein PRO245 cDNA. US2003087385-A1.
                                                                                                                                                                                                                                                                                                ADN14810 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2003087357-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003092115-A1.
                                                                                                                                                           Novel human secreted and transmembrane protein PRO245 cDNA US2003087356-A1.
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3.2e-24;
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54.0%; Pred. No. 3.2e-24;
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                                                                               6.0%; Score 111; DB 11; 54.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Human secreted/transmembrane protein cDNA, #13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADE79565 standard; cDNA; 1295 BP.
Human secreted/transmembrane protein cDNA, #13
US2003130489-A1.
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54.0%; Pred. No. 3
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Human PRO polynucleotide #168.
US2003100087-A1.
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Human PRO polynucleotide #168.
US2003092113-A1.
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Human PRO polynucleotide #168.
US2003203440-A1.
                                                                                                                                         ADN15362 standard; cDNA; 1295 BP.
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Human PRO polynucleotide #168.
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54.0%;
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Best Local Similarity 54.0%;
RESULT 849
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 848
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RESULT 852
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Best Local Similarity
RESULT 853
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                                                                                              Best Local Similarity RESULT 847
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6.0%; Score 111; DB 12; Length 1295; 54.0%; Pred. No. 3.2e-24;
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Local Similarity 54.0%; Pred. No. 3.2e-24;
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6.0%; Score 111; DB 12; Length 1295; 54.0%; Pred. No. 3.2e-24;
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Query Match

Best Local Similarity 54.0%; Pred. No. 3.2e-24;

RESULT 857
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54.0%; Pred. No. 3.2e-24;
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(GETH ) GENENTECH INC.
ery Match
frans similarity 54.0%; Pred. No. 3.2e-24;
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Local Similarity 54.0%; Pred. No. 3.2e-24;
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54.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
                                                                           Human secreted/transmembrane protein cDNA, #13 US2003129592-A1.
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US2003148370-A1.
                                                                                                                                                                                                                                  cDNA encoding human PRO polypeptide #168.
US2003092108-A1.
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US2003092110-A1.
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cDNA encoding human PRO polypeptide #168
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US2003203439-A1.
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US2003194794-A1.
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Human PRO polynucleotide #168.
US2003199054-A1.
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Human PRO polynucleotide #168.
US2003199062-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADE73776 standard; cDNA; 1295 BP
                                                         CDNA; 1295 BP
                                                                                                                                                                                                                 ADE23312 standard; cDNA; 1295 BP
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                  Best Local Similarity
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                                                         ADE73241 standard;
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(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                         6.0%; Score 111; DB 12; Length 1295; 54.0%; Pred. No. 3.2e-24;
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                                Length 1295;
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Beet Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 873
                                                                                                                                                                     Length 1295;
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Novel human secreted and transmembrane protein PRO245 cDNA.
022003199051-Al.
                                                                                                                                                                Query Match
Best Local Similarity 54.0%; Score 111; DB 12;
RESULT 866
CDNA encoding human PRO polypeptide #168.
PD 23-007-2003.
PD GETH) GENENTECH INC.
                                Score 111; DB 12;
Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 870
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 872
                                                                                                                                                                                                                                                                                                                                                                                                                                              6.0%; Score 111; DB 12; 54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 869
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                                                                                ADE99330 standard; cDNA; 1295 BP.
Human secreted/transmembrane protein cDNA, #13.
US2003211576-A1.
(GETH ) GENENTECH INC.
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CDNA encoding human PRO polypeptide #168.
US2003199052-A1.
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23-OCT-2003.
(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                         ADE91077 standard; cDNA, 1295 BP. Human PRO polynucleotide #168. D32003199061-A1. C3-0CT-2003. (GETH ) GENENTECH INC.
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                                Query Match 6.0%;
Best Local Similarity 54.0%;
RESULT 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-NOV-2003.
(GETH ) GENENTECH INC.
23-OCT-2003.
(GETH ) GENENTECH INC.
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...H ) GENENTECH I.

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Best Local Similarity b

RESULT 867

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PA 23-7
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 871
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Query Match 6.0%; Score 111; DB 12; Length 1295; Best Local Similarity 54.0%; Pred. No. 3.2e-24; RESULT 880
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  Length 1295
                                                       ADE91672 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2003199058-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207360-Al.
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PA (GETH ) GENENTECH INC.

Query Match

Best Local Similarity 54.0%; Pred. No. 3.2e-24;

RESULT 878
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PA (GETH ) GENENTECH INC.
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 875
6.0%; Score 111; DB 12;
54.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Human secreted/transmembrane protein cDNA, #13.
US2003211568-A1.
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Human secreted/transmembrane protein cDNA, #13.
US2003180312-A1.
                                                                                                                                                                                                                                                                                                                                                                                           ADG40346 standard; cDNA; 1295 BP.
Human secreted/transmembrane protein cDNA, #13.
US2003225253-A1.
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cDNA encoding human PRO polypeptide #168.
US2003207376-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADG02251 standard; cDNA; 1295 BP.
Human PRO polynucleotide #168.
US2003207352-A1.
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US2003207422-A1.
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RESULT 879
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(GETH ) GENENTECH INC.
ery Match
5 Local Similarity 54.0%;
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GODD/) GODDARD A. (GODO/) GODOWSKI P J. (GURN) GURNEY A L. (MATH/) MATHER J P. (WILL/) WILLIAMS P M. (WOOD/) WOOD W I.
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(GETH ) GENENTECH INC.
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RESULT 881
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Best Local Similarity
Query Match
Best Local Similarity
RESULT 874
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ADG08341 standard; cDNA; 1295 BP.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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 ADG24230 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 888
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Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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cDNA encoding human PRO polypeptide #168.
US2003207359-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADG11284 standard; cDNA; 1295 BP.
cDNA encoding human PRO polypeptide #168.
US2003207357-A1.
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                                                                                                                                                       APP98584 standard; cDNA; 1295 BP.
Human PRO polynucleotide #168.
US2003208055-Al.
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Human PRO polynucleotide #168.
US2003207353-A1.
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Human PRO polynucleotide #168.
US2003207375-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 891
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Best Local Similarity
RESULT 886
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RESULT 889
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Best Local Similarity
RESULT 890
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RESULT 884
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Best Local Similarity
RESULT 887
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RESULT 882
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Length 1295;
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207424-A1.
06-NOV-2003.
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Novel human secreted and transmembrane protein PRO245 cDNA
US2003207389-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA US2203207427-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207350-A1.
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Novel human secreted and transmembrane protein PRO245 CDNA,
US2003207356-Al.
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Local Similarity, 54.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
                                                                                                                                                 ADG15511 standard; cDNA; 1295 BP.
cDNA encoding human PRO polypeptide #168.
US2003219885-A1.
                                                                                                                                                                                                                                                                                                                   ADF96909 standard; cDNA; 1295 BP.
Human PRO polynucleotide #168.
US2003207371-A1.
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Human PRO polynucleotide #168.
US2003207374-A1.
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Human PRO polynucleotide #168.
US2003207423-A1.
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                                         06-NOV-2003.
(GETH ) GENENTECH INC.
iry Match 6.0%;
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Best Local Similarity 54.0%;
RESULT 899
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Best Local Similarity 54.0%;
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Local Similarity 54.0%;
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US2003207420-A1.

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06-NOV-2003.
(GETH ) GENENTECH INC.
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Pred. No. 3.2e-24;
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34.0%; Pred. No. 3.2e-24;
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Novel human secreted and transmembrane protein PRO245 cDNA. US2003194778-A1. 16-OCT-2003. (GETH ) GENENTECH INC.
                                                                                                                                    ADG60876 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
S20032207390-A1.
06-NOV-2003.
(GETH ) GENEWTECH INC.
                                                                                                                                                                                                                                                                                          ADG61980 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207428-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207364-Al.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207365-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207368-A1.
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                                                                              6.0%; Score 111; DB 12; 54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 904
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     6.0%; Score 111; DB 12;
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RESULT 907
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Human secreted/transmembrane protein cDNA, #13.
US2003027145-A1.
(GETB-2003.
(GETH ) GENENTECH INC.
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Human PRO polynucleotide #168.
US2003207358-A1.
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(GETH ) GENENTECH INC.
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RESULT 902
ID ADG61980 standard; CD
DE Novel human secreted
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC
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RESULT 903
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RESULT 909
ID ADG70890 standard;
DE Novel human secrete
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207421-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207419-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207414-Al.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207416-A1.
06-NOV-2003.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207415-Al.
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Novel human secreted and transmembrane protein PRO245 cDNA
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(GETH ) GENENTECH INC.
£27 Match 6.0%; Score 111; DB 12;
5t Local Similarity 54.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
                                                                        Human secreted/transmembrane protein cDNA, #13 US2003027146-A1.
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182003077723-Al.
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RESULT 917
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RESULT 916
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RESULT 910
ID ADG92586 standard;
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06-NOV-2003.
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20-NOV-2003. (GETH ) GENENTECH INC. (GODO/) GODOWSKI P J. (GURN/) GURNEY A L. (MATH.) MATHER J P. (WILL/) WILLIARB P M. (WOOD/) WOOD W I. (GODO) GODOWSKI P J. (GURN/) GURNEY A L. (MATH) MATHER J P. (WILL/) WILLIAMS P M. (WOOD/) WOOD W I. (GETH ) GENENTECH INC. (GETH ) GENENTECH INC. GENENTECH INC. GENENTECH INC. DESNOYERS L. Best Local Similarity RESULT 932 Best Local Similarity RESULT 933 Local Similarity Local Similarity Local Similarity Local Similarity ADI81124 standard; 07-AUG-2003 06-NOV-2003 22-MAY-2003 Query Match Query Match Query Match Query Match Match Query Match Query Match Query Match DESN/) Query 6.0%; Score 111; DB 12; Length 1295; 54.0%; Pred. No. 3.2e-24; Length 1295; Length 1295; Query Match 6.0%; Score 111; DB 12; Length 1295; Best Local Similarity 54.0%; Pred. No. 3.2e-24; Length 1295; Length 1295; Length 1295; Length 1295 Length 1295 AUH12582 standard; cDNA; 1295 BP. Novel human secreted and transmembrane protein PRO245 cDNA. US2003207378-A1. ADG61428 standard; cDNA; 1295 BP. Novel human secreted and transmembrane protein PRO245 cDNA US2003207429-A1. ADG54660 standard; cDNA; 1295 BP. Novel human secreted and transmembrane protein PRO245 cDNA. US2003207367-A1. ADG56316 standard; cDNA; 1295 BP. Novel human secreted and transmembrane protein PRO245 cDNA US2003207366-A1; ADGS9700 standard; CDNA; 1295 BP. Novel human secreted and transmembrane protein PRO245 CDNA 022003207369-A1. Leary Match

Best Local Similarity 54.0%; Score 111; DB 12; Lear

RESULT 95.0%; Pred. No. 3.2e-24;

ID ADH20375 standard; cDNA; 1295 BP.

PD Human secreted/transmembrance

PN US200400553-A1.

PD 08-JAN-20^\* Query Match 6.0%; Score 111; DB 12; Best Local Similarity 54.0%; Pred. No. 3.2e-24; RESULT 925 uuery Match 6.0%; Score 111; DB 12; Best Local Similarity 54.0%; Pred. No. 3.2e-24; RESULT 920 Query Match 6.0%; Score 111; DB 12; Best Local Similarity 54.0%; Pred. No. 3.2e-24; RESULT 922 6.0%; Score 111; DB 12; 54.0%; Pred. No. 3.2e-24; 6.0%; Score 111; DB 12; 54.0%; Pred. No. 3.2e-24; Ouery Match 6.0%; Score 111; DB 12; Best Local Similarity 54.0%; Pred. No. 3.2e-24; RESULT 924 Human secreted/transmembrane protein cDNA, #13. US2004006211-A1. 08-JAN-2004. ADH28515 standard; cDNA; 1295 BP. Human PRO polynucleotide #168. US2003022331-A1. ADG81077 standard, cDNA, 1295 BP. Human PRO polynucleotide #168. US2003194793-A1. ADH07230 standard; cDNA; 1295 BP 06-NOV-2003. (GETH ) GENENTECH INC. 30-JAN-2003. (GETH ) GENENTECH INC. 06-NOV-2003. (GETH ) GENENTECH INC. 06-NOV-2003. (GETH ) GENENTECH INC. (GETH ) GENENTECH INC. 16-OCT-2003. (GETH ) GENENTECH INC. 06-NOV-2003. (GETH ) GENENTECH INC. Query Match
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RESULT 923 (DESN/) DESNOYERS L. Best Local Similarity RESULT 927 Query Match Best Local Similarity RESULT 919 Query Match RESULT 921 ID ADH129 DE NOVEL PN US2003 PD 06-NOV

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Noyel human secreted and transmembrane protein PRO245 cDNA.
US2004009548-Al.
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Local Similarity 54.0%; Pred. No. 3.2e-24;
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14-AUG-2003.
(GETH ) GENENTECH INC.
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Pred. No. 3.2e-24;
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Human secreted/transmembrane protein cDNA, #13.
US2003096340-A1.
                                                                                 Human secreted/transmembrane protein cDNA, #13 US2003215904-A1.
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US2004005665-Al.
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Human secreted/transmembrane protein cDNA, #13
US2003148419-A1.
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US2003207361-A1.
                                                              ADH59775 standard; cDNA; 1295 BP
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Novel human secreted and transmembrane protein PRO245 CDNA.
US2004039164-Al.
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(GETH) GENENTECH INC.
ery Match 6.0%; Score 111; DB 12;
st Local Similarity 54.0%; Pred. No. 3.2e-24;
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Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 946
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 950
                                                                                                               Human secreted/transmembrane protein cDNA, #13. US2003096233-A1. 22-MAY-2003. GF GETH ) GENENTECH INC. 6.0%; Score 111; DB 12; St Local Similarity 54.0%; Pred. No. 3.2e-24;
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Local Similarity 54.0%; Pred. No. 3.2e-24;
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54.0%; Pred. No. 3.2e-24;
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Human secreted/transmembrane protein cDNA, #13
US2003190611-A1.
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cDNA encoding human PRO polypeptide #168.
US2004048333-A1.
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CODA encoding human PRO polypeptide #168.
26-FEB-2004.
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US2004058424-A1.
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Human PRO polynucleotide #13.
US6686451-B1.
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WO2004031105-A2.
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Best Local Similarity 54.0%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                                                                                            Best Local Similarity RESULT 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                      Query Match
Best Local Similarity
RESULT 944
                                                                                               ADM25030 standard;
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RESULT 948
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                                                                                                 Length 1295;
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                                                                                                                                                                                                                                                     6.0%; Score 111; DB 12; Length 1295; 54.0%; Pred. No. 3.2e-24;
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                                                                                                                                                    ADII5338 standard; cDNA; 1295 BP.
MOVel human secreted and transmembrane protein PRO245 cDNA.
US2003207382-A1.
06-NOV-2003.
                                                                                                                                                                                                                                                                                                              ADG09215 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2004009547-Al.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207349-Al.
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Novel human secreted and transmembrane protein PRO245 cDNA
US2003207383-A1.
Leny Match (G.0%; Score 111; DB 12; Len Best Local Similarity 54.0%; Pred. No. 3.2e-24; RESULT 936

ID AD115338 standard; CDNA; 1295 BP.

DE Novel human secreted and trained by US2003207382-A1.

PD OS-NOV-2007
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54.0%; Pred. No. 3.2e-24;
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 939
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Pred. No. 3.2e-24;
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Human secreted/transmembrane protein cDNA, #13.
US2003186358-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADI65692 standard; cDNA; 1295 BP.
Human secreted/transmembrane protein cDNA, #13
US2003148371-A1.
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US2004023331-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity 5
RESULT 942
ID AD099492 standard; cDN
DE Human secreted/transme
PD 02-0CT-2003.
PA (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 941
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Best Local Similarity
RESULT 938
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ADT94236 standard; cDNA; 1295 BP.
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                                                                                                                                                                                                                                                                                          Length 1295;
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207354-Al.
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Best Local Similarity 54.0%; Pred. No. 3.2e-24;
RESULT 958
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Pred. No. 3.2e-24;
                                                                                                                                                                                                                                                                                      6.0%; Score 111; DB 12; 54.0%; Pred. No. 3.2e-24;
     54.0%; Pred. No. 3.2e-24;
                                                                                                                                                                                                             Human secreted/transmembrane protein cDNA, #13.082004137561-A1.
US2004137561-A1.
(GETH ) GENENTECH INC.
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                                     ADM28285 standard; cDNA; 1295 BP.
cDNA encoding human PRO polypeptide #168
US2004077064-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AD195767 standard; cDNA; 1295 BP.
cDNA encoding human PRO polypeptide #168.
US2003077659-A1.
                                                                                                                                                                                             ADR10950 standard; cDNA; 1295 BP
                                                                                                                                                                                                                                                                                                                                                ADR17859 standard; cDNA; 1295 BP
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54.0%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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WILLIAMS P M.
WOOD W I.
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BOTSTEIN D.
DESNOYERS L.
                                                                                                                                                Best Local Similarity RESULT 954
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Best Local Similarity
RESULT 956
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Best Local Similarity
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STEWART T A.
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FILVAROFF E
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Best Local Similarity
RESULT 959
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PAONI N F.
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                                                                                                                                      Query Match
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Best Local
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Tumour-associated antigenic target (TAT) cDNA DNA326887, SEQ ID NO:5879.
WO2004030615-A2.
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Human flavin-containing mono-oxygenase isoform 2 genomic sequence.
WO9824914-A1.
                                                                          Length 1295;
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WO2003025138-A2.
27-WAR-2003.
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Human nervous system related polynucleotide SEQ ID NO 13188.
WO200159063-A2.
                                                                        Query Match 6.0%; Score 111; DB 13;
Best Local Similarity 54.0%; Pred. No. 3.2e-24;
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54.0%; Pred. No. 3.2e-24;
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54.0%; Pred. No. 3.4e-24;
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Pred. No. 3.8e-24;
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(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
Match
6.0%; Score 111; DB 2;
t Local Similarity 80.1%; Pred. No. 2e-23;
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ry Match 6.0%; Score 111; DB 5;
t Local Similarity 80.1%; Pred. No. 1.2e-23;
                                                                                                                                 ADS74498 standard; cDNA; 1295 BP.
Human secreted/transmembrane cDNA #13.
US2004185531-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABA19324 standard; DNA; 27733 BP
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Human PRO245 cDNA sequence. AU2003259607-A1. 27-NOV-2003. (GETH ) GENENTECH INC.
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WILLIAMS P M.
WOOD W I.
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PAONI N F.
ROY M A.
STEWART T A.
                                                                                                                                                                                                                                                                                        FERRARA N.
FILVAROFF E.
                                                                                                                                                                                                                                               DESNOYERS L
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RESULT 962
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ABN89533 standard, DNA, 48436 BP.
Human corneal N-acetylglucosamine-6-sulfotransferase DNA SEQ ID NO:38.
US2002061562-A1.
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DNA sequence of a human immunoglobulin heavy chain variable region.
WO2004029249-A1.
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ry Match
t Local Similarity 80.1%; Pred. No. 7e-23;
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(SAGR-) SAGRES DISCOVERY.
ery Match
ery Match
-- ' ... | Similarity 75.6%; Pred. No. 4.4e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 130207;
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                                                                                                                                                                                                                                                                                                                                   6.0%; Score 111; DB 10; Length 94719; 75.6%; Pred. No. 4.4e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.0%; Score 111; DB 4; Length 160552; 80.1%; Pred. No. 6.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 94720;
                                                                                                                                                                                                           Length 48436;
                                                                  Length 27733
Human nervous system related polynucleotide SEQ ID NO 11655. WO200159061-A2.
                                                                                                                                                                                                                                                                                                                                                                                               Human STATSB carcinoma associated gene, SEQ ID NO:1172 WO2003057146-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD02697 standard; DNA; 160552 BP.
Human glycosyl sulfotransferase-4 (GST-4) genomic DNA.
WO200106015-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    query Match 6.0%; Score 111; DB 11;
Best Local Similarity 80.1%; Pred. No. 5.4e-23;
RESULT 971
                                             (HUMA-) HUMAN GENOME SCI INC.

ry Match

t Local Similarity 80.1%; Pred. No. 2.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 111; DB 9;
Pred. No. 4.4e-23;
                                                                                                                                                                                                         6.0%; Score 111; DB 6;
80.1%; Pred. No. 3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACH93861 standard; DNA; 119 BP.
Human genome derived single exon probe #27056.
US2003194704-Al.
                                                                                                                                                                                                                                                   ADESSO2 standard; DNA; 94719 BP.
Human STATSB gene genomic DNA sequence.
WO20039484-A2.
15-MAY-2003.
(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACN44762 standard; DNA; 130207 BP. Human genomic sequence hCG21349. PCS2030303926-A2. (SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADB72392 standard; DNA; 94720 BP.
Human STAT5B gene.
WO2003008583-A2.
                                                                                                                                                                                                                                                                                                                                                                                  ADA02654 standard; DNA; 94720 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                              17-JUL-2003.
(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
RESULT 970
                                                                                                                                                                                                 Query Match
Best Local Similarity
RESULT 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 972
                                                                                                                                                       23-MAY-2002.
(FUKU/) FUKUDA M N.
(AKAM/) AKAMA T O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                          Best Local Similarity RESULT 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-APR-2004
                                  16-AUG-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JAN-200
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                PAPER
                                                                                                                                                                                                                                                          BBBBB
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AAK87412 standard; DNA; 3504 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42224.
WO200157182-A2.
09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADO85414 standard; cDNA; 6140 BP.
Human tumour-associated antigenic target (TAT) cDNA sequence #2228.
WO2004060270-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              guery Match 6.0%; Score 110.8; DB 11; Length 79590;
Best Local Similarity 79.4%; Pred. No. 4.6e-23;
RESULT 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.0%; Score 110.8; DB 13; Length 6140; 72.5%; Pred. No. 9.7e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.0%; Score 110.8; DB 10; Length 2233; 72.5%; Pred. No. 5.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.0%; Score 110.8; DB 4; Length 3504; 77.1%; Pred. No. 6.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4002;
                                                                                                                                                         Length 128;
                                                                                                                                                                                                                                                                                                                           Length 567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADA03074 standard; DNA; 79684 BP.
Human hCG77579 carcinoma associated gene, SEQ ID NO:1592.
WO2003057146-A2.
                                                                                                                                                                                                                                 Human colon cancer antigen encoding cDNA SEQ ID NO.860.
WO200122920-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADQ97343 standard; DNA; 61739 BP.
Human cancer associated sequence HD08-035, SEQ ID 320.
WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK69827 standard; DNA; 4002 BP.
Human secreted protein gene 14 genomic DNA fragment
WO200226931-A2.
                                                                                                                                                                                                                                                                                        PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 76.8%; Pred. No. 2.3e-24;
RESULT 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MCACCE---
(4-APR-2002.
(HUMA-) HUMAN GENOME SCI INC.
(ery Match
(ery Match 72.5%; Pred. No. 7.5e-24;
                                                                                                                                                         6.0%; Score 110.8; DB 5; 98.2%; Pred. No. 9.1e-25;
RESULT 974

ID AAF65710 standard; cDNA; 128 BP.

DE Novel human polymucleotide, SEQ ID NO: 1466.

PN W0201012568-A2.

PD 11-JAN-2001.

PA (CHIR ) CHIRON CORP.

PA (HYSE-) HYSEQ INC. 6 N*: Score 110.8; !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADL27152 standard; DNA; 79590 BP.
Human genomic sequence for hCG27579 #2.
US2003216558-A1.
                                                                                                                                                                                                                                                                                                                                                                                      ADA53157 standard; cDNA; 2233 BP. Human coding sequence, SEQ ID 725 EP1293569-A2.
                                                                                                                                                                                                                      CDNA; 567 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HELI-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-NOV-2003.
(MORR/) MORRIS D W.
(ENGE/) ENGELHARD E K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC. (WUTD/) WU T D. (ZHOU/) ZHOU Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 977
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 980
                                                                                                                                                                      Best Local Similarity RESULT 975
                                                                                                                                                                                                                      AAH33804 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAR-2003
                                                                                                                                                                                                                                                                                    05-APR-2001
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19-FEB-2004
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                                                                                                                                                             Query Match
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(MERB/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-SEP-2004.
(SAGR-) SAGRES DISCOVERY INC.
ery Match
6.0%; Score 110.8; DB 13; Length 117750;
                                                                                                                                                                                                                                                                                                   vuery Match 6.0%; Score 110.8; DB 10; Length 79684;
Best Local Similarity 79.4%; Pred. No. 4.6e-23;
RESULT 985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12; Length 119501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11; Length 270150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.0%; Score 110.8; DB 11; Length 94330; 81.1%; Pred. No. 5.1e-23;
                                      Length 79684;
                                                                                                                                                                            DB 9; Length 79684;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 526;
                                  Score 110.8; DB 9;
Pred. No. 4.6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-2001.
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
f 0%: Score 110.6; DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.0%; Score 110.8; DB 1;
Best Local Similarity 83.0%; Pred. No. 5.9e-23;
RESULT 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        App65796 standard; DNA; 270150 BP.

Human 16p133 sequence section 7 of 8 DNA.

W02003072827-A1.

W02003072827-A1.

G04-SEP-2003.

(CHLL-) CHILDREN'S HOSPITAL MEDICAL CENT.

6.0%; Score 110.8; DB 11

ELocal Similarity 72.5%; Pred. No. 9.8e-23;
                                                                                                                                                                        Ouery Match 6.0%; Score 110.8; DB 9
Best Local Similarity 79.4%; Pred. No. 4.6e-23;
RESULT 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.0%; Score 110.6; DB 5 79.8%; Pred. No. 2.5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.0%; Score 110.6; DB 5 79.8%; Pred. No. 2.5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABD32653 standard; DNA; 117750 BP.
Human cancer-associated genomic DNA HD13-060.
WO2004074320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                   ADA66358 standard; DNA; 79684 BP.
Human hCG27579 gene genomic DNA sequence.
MOJUL-2003.
(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADL37082 standard; DNA; 526 BP.
Human ovarian cancer DNA marker #10972.
WO200170979-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADL43466 standard; DNA; 584 BP.
Human ovarian cancer DNA marker #17356.
W0200170999-A2.
27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADI71931 standard; DNA; 526 BP.
Human ovarian cancer DNA marker #4673.
WO200170979-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AD129095 standard; DNA; 119501 BP.
Human MARK3 genomic DNA.
US2003232771-A1.
                                                                                                                                                                                                                                                                                                                                                                   ACN44662 standard; DNA; 94330 BP. Human genomic sequence hCG20930. Mo20030073826-A2. 12-SEP-2003. (SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                              ADB72812 standard; DNA; 79684 BP
PD 17-JUL-2003.

PA (SAGR-) SAGRES DISCOVERY.

Query Match

6.0%;

Best Local Similarity 79.4%;

RESULT 983
                                                                                                                                                                                                                                                                             30-JAN-2003.
(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-DEC-2003.
(ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human hCG27579 gene.
WO2003008583-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
RESULT 987
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Best Local Similarity
RESULT 986
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ACN39479 standard; cDNA; 1341 BP.
Tumour-associated antigenic target (TAT) cDNA DNA325690, SEQ ID NO:3643.
WO2004030615-A2.
                                                                                                                                                                 .Match 6.0%; Score 110.6; DB 13; Length 1341;
Local Similarity 78.7%; Pred. No. 4.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 110.6; DB 10; Length 1697; Pred. No. 5.1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.0%; Score 110.6; DB 13; Length 1697; 78.7%; Pred. No. 5.1e-24;
                                                                                                                                                                                                                                                                                                                    Length 1388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 110.6; DB 2; Length 2791; Pred. No. 6.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.0%; Score 110.6; DB 4; Length 2791; 78.7%; Pred. No. 6.9e-24;
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
6.0%; Score 110.6; DB 5; Length 584;
it Local Similarity 79.8%; Pred. No. 2.7e-24;
                                                                                                                                                                                                                                                                                                     vuery Match 6.0%; Score 110.6; DB 12;
Best Local Similarity 78.7%; Pred. No. 4.5e-24;
RESULT 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.0%; Score 110.6; DB 6; 78.7%; Pred. No. 4.7e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE08775 standard; DNA; 1697 BP.
Novel DNA-related contig nucleotide sequence #19
WO2003054152-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AASS9232 standard; cDNA; 2791 BP.
Human cDNA encoding a secreted protein yc2_1.
WO200175068-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADS11156 standard; DNA; 1697 BP.
Human therapeutic contig DNA - SEQ ID 1393.
WO2004080148-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX80486 standard; cDNA; 2791 BP.
Human secreted protein yc2_1 encoding cDNA.
WO9932614-A1.
                                                                                                                                                                                                                      ADKO0610 standard; DNA; 1388 BP.
HOMO protein encoding sequence #11
WO2004014946-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABA90901 standard; cDNA; 2791 BP.
Human polynucleotide SEQ ID NO 51
US2001039335-Al.
                                                                                                                                                                                                                                                                                                                                                                    ABO99278 standard; cDNA; 1472 BP. Human coding sequence SEQ ID 11. W0200259260-A2. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WOYSSECTOR O1-JUL-1999.
(GEMY ) GENETICS INST INC.
(GEMY MAtch
...ilarity 78.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.0%;
78.7%;
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LAVALLIE E R.
COLLINS-RAÇIE L A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-OCT-2001.
(GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TREACY M.
AGOSTINO M J.
STEININGER R J.
                                                                                                                                                   GENENTECH INC.
                                                                                                                                                                                                                                                                                                   (NEWO-) NEWORGEN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-SEP-2004.
(NUVE-) NUVELO INC.
                                  Best Local Similarity RESULT 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 996
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Best Local Similarity
RESULT 997
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(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (JACO/) JACOBS K.
(MCCO/) MCCOY J M.
(LAVA/) LAVALLIE B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TREA/) (AGOS/) (STEI/)
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Lougth 3775;

Lough 3775;

Lough 3775;

PD 16-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match

Got; Score 110.6; DB 5; Length 12328;

RESULT 1002

ID ADC60735 standard; DNA; 50000 BP.

DE Human slingshot-related DNA 9.

PD 08-APR-2003

PD 08-APR-2003

PA (F.A.C.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 110000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.0%; Score 110.6; DB 11; Length 141586; 80.4%; Pred. No. 7.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD56274 standard; DNA; 99100 BP.
Human cyclin-dependent kinase 10, CDK10, genomic sequence.
Juery Match
6.0%; Score 110.6; DB 12; Length 99100;
lest Local Similarity 80.4%; Pred. No. 6.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 79544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.0%; Score 110.6; DB 3; Length 138169;
Best Local Similarity 80.4%; Pred. No. 7.5e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 110.6; DB 3; Length 141589;
Pred. No. 7.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 50000;
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Human adenosine receptor related polynucleotide SEQ ID NO:2480.
W020009525-A2.
24-FEB-2000.
(UYEC-) UNIV EAST CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA35005 standard; DNA; 141589 BP.
Human adenosine receptor related polynucleotide SEQ ID NO:2694.
WO200009525-A2.
                                                                                                                                           6.0%; Score 110.6; DB 6; Length 2791; 78.7%; Pred. No. 6.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADQ97764 standard; DNA; 79544 BP.
Human cancer associated sequence HD10-042, SEQ ID 741.
WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUL-2004.
(SACR-) SAGRES DISCOVERY INC.
(SACR-) SAGRES DISCOVERY INC.
6.0%; Score 110.6; DB 12;
ery Match
78.7%; Pred. No. 5.4e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 110.6; DB 11;
Pred. No. 6.6e-23;
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Pred. No. 6.6e-23;
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ID ABD20695 standard; DNA; 141586 BP.
DE Human pulmonary and inflammatory target DNA #306
PD 90200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.0%; Score 110.6; DB 1
75.8%; Pred. No. 4.1e-23;
                                                                                                                                                                                                                                                AAI61061 standard; cDNA; 3775 BP.
Human polynucleotide SEQ ID NO 5050.
WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-2002,
(EPIG-) EPIGENESIS PHARM INC.
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84.2%;
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84.2%;
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A (UTEC-) UNIV EAST CAROLINA.
G (OB-Y) MATCH
Best Local Similarity 80.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002.
2002.
2002.
AG-) EPIGENESIS F.
EXY Match
Best Local Similarity 8, RESULT 1009
ID AAA35005 standar
DE Human adence Physical No. 200000 Physical Physica
(SPAU/) SPAULDING V. (WONG/) WONG G G. (CLAR/) CLARK H. (FECH/) FECHTEL K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 1003
                                                                                                                                                                         Best Local Similarity RESULT 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 1004
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Best Local Similarity
RESULT 1006
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Best Local Similarity
RESULT 1007
                                                                                                                                                                                                                                                                                                                                                          26-JUL-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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AAF21152 standard; DNA; 141589 BP.
Human low adenosine antisense oligonucleotide related sequence #2719.
WO200062736-A2.
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Human low adenosine antisense oligonucleotide related sequence #2694.
WO200062736-A2.
26-OCT-2000.
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PA (BPIG-) EPIGENESIS PHARM INC.
Query Match 6.0%; Score 110.6; DB 10; Length 141589;
Best Local Similarity 80.4%; Pred. No. 7.7e-23;
RESULT 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 110.6; DB 10; Length 141589; Best Local Similarity 80.4%; Pred. No. 7.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-OCT-2002.
(BFIG-) EPIGENESIS PHARM INC.
(ery Match 6.0%; Score 110.6; DB 10; Length 141589;
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( [EPIG-) EPIGENESIS PHARM INC.

Query Match 6.0%; Score 110.6; DB 11; Length 141589;

Best Local Similarity 80.4%; Pred. No. 7.7e-23;
                                                                                                                                                                                                                                                                                                                                           6.0%; Score 110.6; DB 3; Length 141589; 80.4%; Pred. No. 7.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.0%; Score 110.6; DB 3; Length 141589; 80.4%; Pred. No. 7.7e-23;
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                                                                                                                                Length 141589
ID AAA35030 standard; DNA; 141589 BP.

ID AAA35030 standard; DNA; 141589 BP.

BY WO200009525-A2.

PD 24-FEB-2000.

PA (UYEC.) UNIV EAST CAROLINA.

Query Match 6.0%; Score 110.6; DB 3; Length 141589

Best Local Similarity 80.4%; Pred. No. 7.7e-23;

RESULT 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABD20670 standard; DNA; 141589 BP.
Human pulmonary and inflammatory target DNA #281
WO200285309-A2.
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 80.4%; Score 110.6; RESULT 1012
ID AAR20913 standard; DNA; 141589 BP.
DE Human ELAM-1 polynucleotide fragment #2480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jr 1018
MaD19162 standard; DNA; 141601 BP.
Human ELAM-1 DNA fragment #2.
WO200285309-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABZ96821 standard; DNA; 141589 BP.
Human nucleic acid sequence.
WO200285308-A2.
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Human nucleic acid sequence.
WO200285308-A2.
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Human ELAM-1 nucleic acid.
WO200285308-A2.
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                                                                                                                                                                                                                                                                                                  (UYEC-) UNIV EAST CAROLINA. (NYCE/) NYCE J W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYEC-) UNIV EAST CAROLINA (NYCE/) NYCE J W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 1017
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Best Local Similarity
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(HUMA-) HUMAN GENOME SCI INC.
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PD 31-0CT-2002.

PA (EPIG-) EPIGENESIS PHARM INC.

Query Match

Best Local Similarity 80.4%; Pred. No. 9.7e-23;

RESULT 1024

ID ABD17970 standard; DNA; 209284 BP.

DE Human factor-related antisense pol---

PD 31-0CT-2002.

PD 31-0CT-2002.

PA (EPIG-) EPIGENESIS PHARM INC.

G.0%; Score 110.6; DB 10; Length 209274;

RESULT 1024

ID ABD17970 standard; DNA; 209284 BP.

DE Human factor-related antisense pol---

PD 31-0CT-2002.

PA (FILT.)
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Human musculoskeletal system related polynucleotide SEQ ID NO 788.
WO200155367-Al.
02-AUG-2001.
6.0%; Score 110.6; DB 11; Length 141601; 80.4%; Pred. No. 7.7e-23;
                                                                                                                                                                                                                                                                                                                                                      vuery Match 6.0%; Score 110.6; DB 10; Length 146982; Best Local Similarity 80.4%; Pred. No. 7.8e-23; RESULT 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11; Length 146984;
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ry Match
t Local Similarity 80.4%; Pred. No. 9.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.0%; Score 110.6; DB 11; Length 248436; 77.2%; Pred. No. 1.1e-22;
                                                                                                                                                                                           6.0%; Score 110.6; DB 3; Length 146981; 80.4%; Pred. No. 7.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 110.4; DB 11; Length 22021; Pred. No. 2.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human factor-related antisense polynucleotide #3004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.0%; Score 110.6; DB 1380.4%; Pred. No. 7.8e-23;
                                                             AAF21442 standard; DNA; 146981 BP.
Human ELAM-1 polynucleotide fragment #3009.
WO200062736-A2.
                                                                                                                                                                                                               Best Local Similarity 80.4%; Pred. No. 7 RESULT 1020
ID ABZ97136 standard; DNA; 146982 BP. Prod. No. 1738. PN WO200255308-A2. PN WO200255308-A2. PA (EPIG-2002. PA (EPIG-2002.)
                                                                                                                                                                                                                                                                                                                                                                                                                                     ABD19160 standard; DNA; 146984 BP.
Human BLAM-1 DNA fragment 1738.
WO200285309-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACN45190 standard; DNA; 248436 BP.
Human genomic sequence hCG16330.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF21437 standard; DNA; 209273 BP
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Human genomic sequence hCG20786.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-2002.
(EPIG-) EPIGENESIS PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-OCT-2000.
(UYEC-) UNIV EAST CAROLINA.
(NYCE/) NYCE J W.
                                                                                                                             26-OCT-2000.
(UYEC-) UNIV EAST CAROLINA.
(NYCE/) NYCE J W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-SEP-2003. (SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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RESULT 1027
Query Match
Best Local Similarity
RESULT 1019
ID AAF21442 standard; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
RESULT 1025
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Best Local S
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ADJ12650 standard; DNA; 16422 BP.
DNA fragment of a BAC clone that encodes a human secreted protein Seg504.
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A (SAGR-) SAGRES DISCOVERY.

Query Match

Best Local Similarity 80.7%; Pred. No: 4.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.0%; Score 110.2; DB 12; Length 16422; 80.7%; Pred. No. 2.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 21581;
                                                                                                                                                                                                                                                                                 ADJ28161 standard; DNA; 612 BP.
Human musculoskeletal system-associated contig DNA - SEQ ID 788.
US2004009488-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD 27-MAY-2004.

PA (GETH ) GENENTECH INC.

Query Match

G.0%; Score 110.2; DB 12; Length 6905;

Best Local Similarity 80.7%; Pred. No. 1.6e-23;

RESULT 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PD 29-JUN-1995.

PA (IMMU-) IMMUNOBIOLOGY RES INST INC.

Query Match 6.0%; Score 110.2; DB 2; Length 6905;

Best Local Similarity 80.7%; Pred. No. 1.6e-23;

RESULT 1031
                                                                                                                                                                                                                                                                                                                                              IS-JAN-2004.
(HUMA-) HUMAN GENOME SCI INC.
ery Match
for match (18) Score 110.2; DB 12; Length 612;
for match (18) Pred. No. 3.7e-24;
                                                           ABX58434 standard; cDNA; 612 BP.
cDNA encoding novel human musculoskeletal system antigen #778.
US2002147140-Al.
6.0%; Score 110.2; DB 4; Length 612; 80.7%; Pred. No. 3.7e-24;
                                                                                                                                                                                                                          Length 612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ID ADC87234 standard; DNA; 21581 BP.

DE Human GPCR gene SEQ ID NO:1687.

PN BP127024-A2.

PD 02-JAN-2003.

PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

Query Match

6.0%; Score 110.2; DB 10;

Best Local Similarity 74.7%; Pred. No. 3.3e-23;

RESULT 1034
                                                                                                                                                                                                                          DB 8;
                                                                                                                                                                                                                      6.0%; Score 110.2; DB 8 80.7%; Pred. No. 3.7e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ92779 standard; DNA; 6905 BP.
Human thymopoietin continuous gene fragment.
WO9517205-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACN43878 standard, DNA, 39148 BP.
Human genomic sequence hCG36720.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADO19382 standard; DNA; 6905 BP.
Human PRO polymucleotide #720.
WO2004043361-A2.
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FLORENCE K A.
GREENE J M.
                                                                                                                             10-OCT-2002.
(ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
               Best Local Similarity RESULT 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (YOUN/) YOUNG P E.
(FERR/) FERRIE A M.
(YUGG/) YU G.
(FLOR/) FLORENCE C.
(EBNE/) BENER R.
(OLSE/) OLSEN H.
                                                                                                                                                                                                                                   Best Local Similarity RESULT 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
RESULT 1033
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 1030
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DUAN R D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2004010132-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JAN-2004
(ROSE/) ROS
                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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(GREE/)
(YOUN/)
(FERR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DUAN/)
(RUBE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BREW/)
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(PATH-) PATHOARRAY GMBH.
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RESULT 1047
                   Query Match
Best Local Similarity
RESULT 1044
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RESULT 1051
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAL36242 standard; DNA; 5199 BP.
Human musculoskeletal system related polynucleotide SEQ ID NO 2607.
WO200155367-A1.
                                                                                                                                                    AAL16240 standard; DNA; 5157 BP.
Human musculoskeletal system related polynucleotide SEQ ID NO 2605.
WO200155367-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human musculoskeletal system-associated genomic DNA - SEQ ID 2605. US2004009488-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human musculoskeletal system-associated genomic DNA - SEQ ID 2607.
US2004009488-A1.
ABX59230 standard; cDNA, 5199 BP.
CDNA encoding novel human musculoskeletal system antigen #1574.
US2002147140-A1.
10-OCT-2002.
(ROSE), ROSEN C A.
(RUBE), RUBEN S M.
(BARA), BARASH S C.
                                                                                                                                                                                                                                                                                         ABX55228 standard; cDNA; 5157 BP.
cDNA encoding novel human musculoskeletal system antigen #1572.
US2002147140-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JAN-2004.
(HUMA-) HUMAN GENOME SCI INC.
(ery Match
ery Match
(ery Match 10, DB 12; Length 5199;
(ery Match 10, DB 12; Length 5199;
(ery Match 10, DB 12; Length 5199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 16707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 80.0%; Pred. No. 1.6e-23;
                                                                                                                                                                                                                                             Length 5157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 5199;
                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
ry Match 6.0%; Score 110; DB 4;
t Local Similarity 80.0%; Pred. No. 1.6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
6.0%; Score 110; DB 4;
ery Match 6.0%; Pred. No. 1.66-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.0%; Score 110; DB 8;
80.0%; Pred. No. 1.6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                 6.0%; Score 110; DB 8;
80.0%; Pred. No. 1.6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.0%; Score 110; DB 2; 76.9%; Pred. No. 3.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACA64895 standard; DNA; 134292 BP.
Human GABBR1 DNA corresponding to AL031983.
DE10127572-A1.
05-DEC-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAXS8061 standard; DNA; 16707 BP.
Genomic DNA for Human GABAB receptors
WO9921890-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADJ29978 standard; DNA; 5157 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADJ29980 standard; DNA; 5199 BP
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JSG-A1.

JAA-) HUMAN GENON.

JCY MATCh

JESULT 1040

ID ABX99230 standard

DE CDNA encoding

PN US20021471,0

PD 10-OCT-7

PA (ROSP

PA (P)
                                                                                                                                                                                                                                                                                                                                                     , JEN C A.

AAA/) BARASH S C.

ATY MATCH
BEST LOCAL SIMILATITY B.

RESULT 1038
ID ADJ29978 stand**
DE Human musc**
PN US2004**
PD 15-
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Best Local Similarity
RESULT 1043
ID ACA64895 star<sup>2</sup>
DE Human Gar
                                                                                                                                                                                                                                                                                                                                            10-OCT-2002.
(ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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Best Local Similarity
RESULT 1042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
RESULT 1041
                                                                                                                                                                                                         02-AUG-2001
                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                       RESULT 1037

1D ABX59226

DE CDNA enc
PN US20021-
PD 10-OCT---
PA (ROBE/)

PA (RUBE/)

PA (RABE/)
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AAL36258 standard; DNA; 32193 BP.
Human musculoskeletal system related polynucleotide SEQ ID NO 2623.
WO200155367-A1.
                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 69.3%; Pred. No. 3.1e-23;
RESULT 1046
ID AAK89916 standard; DNA; 12288 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3492.
PD 02-AUG-2001.
PA (HUMA-) HIMAN COLLISE STATES BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAK89915 standard; DNA; 14484 BP.
Human digestive system antigen genomic sequence SEQ ID NO: 3491.
WO200155314-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAK89917 standard; DNA; 14495 BP.
Human digestive system antigen genomic sequence SEQ ID NO: 3493.
WO200155314-A2.
02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vuery match
best Local Similarity 69.3%; Pred. No. 3.4e-23;
BESULT 1050
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A (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.0%; Score 109.8; DB 4; Length 32193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.0%; Score 109.8; DB 4; Length 12288; 69.3%; Pred. No. 3.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 14484;
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  Length 134292;
                                                                                                                                                      PD 25-WAR-1999.

PA (GETH) GENENTECH INC.

Query Match
6.0%; Score 109.8; DB 2; Length 114;
Best Local Similarity 97.4%; Pred. No. 1.8e-24;
RESULT 1045
ID ABA07271 standard; DNA; 12288 BP.
                                                                                                                                                                                                                                                                                 ABA07271 standard; DNA; 12288 BP.
Human pancreatic cancer related genomic DNA, SEQ ID NO:
W0200155206-A1.
02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ery Match
6.0%; Score 109.8; DB 4; Length
st Local Similarity 69.3%; Pred. No. 3.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABA07270 standard; DNA; 14484 BP.
Human pancreatic cancer related genomic DNA, SEQ ID NO:
WO200155206-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PD 02-AUG-2001.

Query Match HUMAN GENOME SCI INC.

Query Match Ach 6.0%; Score 109.8; DB 4; Les Best Local Similarity 69.3%; Pred. No. 3.4e-23; RESULT 1049

ID ABAGOT72 standard; DNA, 14495 BP.

DE Human pancreatic cancer related genomic DNA, SEQ ID PN WO200155206-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human novel protein-encoding gene 7, SEQ ID NO:37. 02-AUG-2001.
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PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 6.0%; Score 109.8; DB 4;

Best Local Similarity ' 69.3%; Pred. No. 3.4e-23;

RESULT 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.0%; Score 109.8; DB 4; 79.6%; Pred. No. 5.6e-23;
  Score 110; DB 8;
Pred. No. 1.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD16595 standard; DNA; 32193 BP
                                                                        AAX56603 standard; DNA; 114 BP.
Human 345566 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
6.0%;
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(HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-FEB-200
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                                                                                                                                                                                   Query Match
                        Query Match
                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Luery Match 6.0%; Score 109.8; DB 9; Length 79684; Best Local Similarity 79.3%; Pred. No. 9.8e-23; RESULT 1058

ID ADA66358 standard; DNA; 79684 BP.

DE Human hCG27579 gene genomic DNA 79684 BP.

PN WC2003053224-A2.

PD 03.JUL-2001
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Human musculoskeletal system related polynucleotide SEQ ID NO 2713.
WO200155367-Al.
02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                        Human musculoskeletal system-associated genomic DNA - SEQ ID 2623
US2004009488-A1.
                                                                                                                                                                                                                                                              vuery Match 6.0%; Score 109.8; DB 10, Length 32193;
Beet Local Similarity 79.6%; Pred. No. 5.6e-23;
RESULT 1055
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ry Match

t Local Similarity 79.6%; Pred. No. 5.6e-23;
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                                ABX59246 standard; cDNA; 32193 BP.
cDNA encoding novel human musculoskeletal system antigen #1590.
US2002147140-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9; Length 79684;
                                                                                                                                                Length 32193,
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Human protein phosphatase 2A alpha subunit 22. 66,
CN1355310-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.0%; Score 109.6; DB 10; 78.4%; Pred. No. 1e-23;
                                                                                                                                                6.0%; Score 109.8; DB 8; 79.6%; Pred. No. 5.6e-23;
                                                                                                                                                                                                             Genomic DNA encoding human NOVX protein seq id 37 US2003207285-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 109.8; DB 9
Pred. No. 9.8e-23;
      79.6%; Pred. No. 5.6e-23;
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Pred. No. 9.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.0%; Score 109.8; DB 1 79.3%; Pred. No. 9.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genomic sequence for hCG27579 #2. US2003216558-A1.
                                                                                                                                                                                              ADG62943 standard; DNA; 32193 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB72812 standard; DNA; 79684 BP. Human hCG27579 gene. WC2003008583-A2. 30-JAN-2003.
                                                                                                                                                                                                                                                                                                                           DNA; 32193 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADL27152 standard; DNA; 79590 BP
                                                                                                                                                                                                                                         06-NOV-2003.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.0%;
Best Local Similarity 79.3%;
RESULT 1057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MORR/) MORRIS D W. (ENGE/) ENGELHARD B K.
                                                                                                                                                            Best Local Similarity RESULT 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 1060
                                                                                                (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
Best Local Similarity
RESULT 1053
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JUN-2002.
(UYFU-) UNIV FUDAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
RESULT 1061
                                                                                                                                                                                                                                                                                                                         ADJ29996 standard;
                                                                                                                                                                                                                                                                                                                                                                         15-JAN-2004
                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                     DA PO PE
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Human musculoskeletal system-associated genomic DNA - SEQ ID 2713 US2004009488-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 37904;
                                                                                                                                                                                                                                                                                                                                                                                                                                     6.0%; Score 109.6; DB 12; Length 19820; 74.5%; Pred. No. 4.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID ABK87217 standard; DNA; 30709 BP.

DB Human lipase, hormone-sensitive (LIPE) gene sequence.

Query Match 6.0%; Score 109.6; DB 6; Length 30709;

Best Local Similarity 78.6%; Pred. No. 6.3e-23;
                                                                      ABX59336 standard; cDNA; 19820 BP.
cDNA encoding novel human musculoskeletal system antigen #1680.
US2002147140-A1.
  4; Length 19820;
                                                                                                                                                                                                                                              8; Length 19820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PA (HELL-) HELIX RES INST.

Query Match

Best Local Similarity 79.6%; Pred. No. 8.8e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PA (HELL-) HELIX RES INST.

Query March
5.9%; Score 109.4; DB 4; Length 573;
Best Local Similarity 79.6%; Pred. No. 6.4e-24;
RESULT 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match
6.0%; Score 109.6; DB 10;
Best Local Similarity 77.1%; Pred. No. 7.2e-23;
RESULT 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-AUG-2001.
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
BY MARCH
5.9%; Score 109.4; DB 5;
st Local Similarity 98.4%; Pred. No. 6.3e-24;
                                                                                                                                                                                                                                           6.0%; Score 109.6; DB 8 74.5%; Pred. No. 4.8e-23;
6.0%; Score 109.6; DB 4 74.5%; Pred. No. 4.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH00279 standard; cDNA; 573 BP.
Human cDNA clone (3'-primer) SEQ ID NO:6114.
EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABV00481 standard; cDNA; 550 BP.
Human prostate expression marker cDNA 3472.
WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADD72117 standard; cDNA; 3600 BP.
Human endozepine-like protein NOV1c cDNA.
US2003195149-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH18360 standard; cDNA; 949 BP.
Human cDNA sequence SEQ ID NO:18397.
EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACN44966 standard; DNA; 125534 BP.
Human genomic sequence hCG32986.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                               ADJ30086 standard; DNA; 19820 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC87244 standard; DNA; 37904 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human GPCR gene SEQ ID NO:1697.
EP1270724-A2.
                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-2004.
(HUMA-) HUMAN GENOME SCI INC.
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(SAGR-) SAGRES DISCOVERY.
                                                                                                                                            10-OCT-2002.
(ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                    Best Local Similarity
RESULT 1062
                                                                                                                                                                                                                                                        Best Local Similarity
RESULT 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 1064
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Best Local Similarity
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Decomposition of the control of the 
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Query Match
Best Local Similarity 71.5%; Score 109.4; DB 6; Length 3920;
RESULT 1075
ID AAL43758 standard; DNA; 3920 BP.
DE Human NOV1e gene sequence.
PN WO200244211-A2.
PD 06-JUN-200?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10; Length 3682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.9%; Score 109.4; DB 10; Length 3920; 71.5%; Pred. No. 2.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query March 5.9%; Score 109.4; DB 6; Length 3920; Best Local Similarity 71.5%; Pred. No. 2.1e-23; RESULT 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 109.4; DB 6; Length 3887; Pred. No. 2.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.9%; Score 109.4; DB 6; Length 3920; 71.5%; Pred. No. 2.1e-23;
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Human flavin containing monooxygenase-2 (FMO2) gene sequence.
WO200253579-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADD72116 standard; cDNA; 3920 BP.

Human endozepine-like protein NOV1a cDNA NOV1b.
US2003195149-A1.
16-OCT-20031
(GANG/) GANGOLLI E A.
(STON/) STONE D J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 109.4; DB 6
Pred. No. 2.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JANN-2003.

(KAZU-) ZH KAZUSA DNA KENKYUSHO.

(RAZU-) PROTEIN EXPRESS KK.

(PROT-) PROTEIN EXPRESS KK.

S.9%; Score 109.4; DB

Query Match

S.9%; Pred. No. 2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAL43754 standard; DNA; 3887 BP. Human NOV1a gene sequence. Woo200244211-A2. 06-JUN-2002. (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAL43757 standard; DNA; 3920 BP.
Human NOV1d gene sequence.
WO200244211-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAL43755 standard; DNA; 3920 BP.
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Best Local Similarity 71.5%; Pr
RESULT 10.78
ID ADD'2116 standard; CDNA; 3920 B
DE Human endozepine-like protein N
PN US2003195149-A1.
PD 16-OCT-2003.
PA (GANG/) GANGOLLI B A.
PA (STON/) STONE D J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.9%;
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2002.
2AA2.
2AA-) CURAGEN CORP
ETY MATCh
Best Local Similarity 73
RESULT 1076
ID AAL43755 standa-
DE Human NOV1h
PD 06-
PD 06-
PA
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(CURA-) CURAGEN CORP.
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RESULT 1079
ID ABK99191 standard; DN
DE Human flavin containi
PN W0200253579-A2.
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RESULT 1073
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Best Local Similarity
RESULT 1074
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AAD11633 standard; CDNA; 1458 BP.

Human secreted protein-encoding gene 4 cDNA clone HAMGG68, SEQ ID NO:14.

WC200151504-A1.

19-JUL-2001.
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Human immune/haematopoietic antigen genomic sequence SEQ ID NO:31395.
WO200157182-A2.
                                                                                                     ADB16927 standard; DNA; 49806 BP.
Human DYXC1 DNA, chromosomal gene region nucleotides 50001-100000.
WO2003068814-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PD 22-JUL-2004.

PA (SAGR-) SAGRES DISCOVERY INC.

Query Match 5.9%; Score 109.4; DB 12; Length 257645;

Best Local Similarity 79.6%; Pred. No. 2.7e-22;

RESULT 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Guery Match

Best Local Similarity 78.9%; Pred. No. 1e-23;

RESULT 1084

ID AAZ98020 standard; CDNA, 1458 BP.

DE Human secreted protein encoding nucleotide sequence SEQ ID NO:14.

PN W0200004140-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.9%; Score 109.4; DB 13; Length 96256; Best Local Similarity, 75.1%; Pred. No. 1.5e-22; RESULT 1082
                                             Length 28506;
                                                                                                                                                                                                                                              Length 49806;
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(HUMA-) HUMAN GENOME SCI INC.
6-P Match 5.9%; Score 109.2; DB 6; Length 1458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
ry Match
5.9%; Score 109.2; DB 4; Length 1458;
t Local Similarity 72.1%; Pred. No. 1.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.9%; Score 109.2; DB 8; Length 1458; 72.1%; Pred. No. 1.3e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266.
                                                                                                                                                                                                             Best Local Similarity 79.6%; Score 109.4; DB 9; RESUT 10cal Similarity 79.6%; Pred. No. 9.8e-23; ID ADR53001 standard; DNA; 96256 BP.

DE Drug therapy altered expressed gene #352.

PN W02004072265-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADQ97289 standard; DNA; 257645 BP.
Human cancer associated sequence HDO8-026, SEQ ID
WO2004060304-A2.
                                           Query Match 5.9%; Score 109.4; DB 6; Best Local Similarity 79.6%; Pred. No. 7e-23; RESULT 1080
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(HUWA-) HUMAN GENOME SCI INC.

5.9%; Score 109.2; DB 3;

cery Match

72.1%; Pred. No. 1.3e-23;
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ID ADA39556 standard; CDNA; 1458 BP.
DE Human secreted protein encoding CDNA. PP. WC2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-), HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK69729 standard; cDNA; 1458 BP.
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11-JUL-2002.
(GENA-) GENAISSANCE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (BURC/) BURCZYNSKI M.
(TWIN/) TWINE N.
(DORN/) DORNER A J.
(TREP/) TREPICCHIO W L.
                                                                                                                                                                                           21-AUG-2003.
(LICN ) LICENTIA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 1085
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Human secreted protein-related DNA sequence - SEQ ID No 259
                                                                                                                                                                                                                                                                                                     DNA; 128668 BP.
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Human therapeutic DNA - SEQ ID 29.
WO2004080148-A2.
                                                                                                                                                                                                                                                                                                                    Human genomic sequence hCG40471.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                               WOZOUSU.
12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
erv Match
                      WO200277188-A2.
03-OCT-2002.
(HUMA-) HUMAN GENOME SCI INC.
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(NUVE-) NUVELO INC.
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Best Local Similarity
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RESULT 1103
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                                                                                                                                                                                                                                                                                                   ACN44074 standard;
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Best Local Similarity
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                                                                                                                                                                                                                                                      Ouery Match 5.9%; Score 109.2; DB 10; Length 1784; Best Local Similarity 80.3%; Pred. No. 1.5e-23; RESULT 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
(FLY Match 5.9%; Score 109.2; DB 4; Length 32134;
ery Match 82.4%; Pred. No. 8.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.9%; Score 109.2; DB 4; Length 31931; 78.9%; Pred. No. 8.7e-23;
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                                                                                                   Length 1458;
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Human reproductive system related antigen DNA SEQ ID NO: 6763
WO200155320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABA07160 standard; DNA; 31931 BP.
Human pancreatic cancer related genomic DNA, SEQ ID NO: 479.
WO200155206-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1095

ID ABA15813 standard; DNA; Score 109.2; DB 5; Length 3
DB Human nervous system related polynucleotide SEQ ID NO 8144.
PD 16-AUG-2001.
PA (HUMA-) HIMAN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABAIS354 standard; DNA; 32134 BP.
Human nervous system related polynucleotide SEQ ID NO 7685.
WO200159063-A2.
                                             PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 72.1%; Pred. No. 1.3e-23;
RESULT 1089
                  Human secreted protein coding sequence, SEQ ID 26 WO200295010-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
Query Match
5.9%; Score 109.2; DB 5;
Best Local Similarity 82.4%; Pred. No. 8.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.9%; Score 109.2; DB 5; 82.4%; Pred. No. 8.7e-23;
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Human secreted protein-related DNA sequence #84.
91 NO.20292787-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.9%; Score 109.2; DB 1080.3%; Pred. No. 2.1e-23;
                                                                                                                                                ADE72775 standard; DNA; 1784 BP.
Human endometrial specific gene, SEQ ID NO 215.
WQ2003060081-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADE72772 standard; DNA; 3199 BP.
Human endometrial specific gene, SEQ ID NO 212.
                                                                                                                                                                                                                                                                                                             ADO64092 standard, cDNA, 2385 BP. Novel human cDNA sequence #1253. BP1440981-A2. 28-JUL-2004. (REAS-) RES ASSOC BIOTECHNOLOGY.
ACC50359 standard; cDNA; 1458 BP.
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2004.
2004.
2007.
2008.
2008.
Best Local Similarity 7
RESULT 1091
ID ADB72772 stander
DE Human endom
PN WO20030.
PD 24-7
                                                                                                                                                                                                                  24-JUL-2003.
(DIAD-) DIADEXUS INC.
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(DIAD-) DIADEXUS INC.
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RESULT 1097
ID ABT16905 standard: D
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Best Local Similarity
RESULT 1093
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Best Local Similarity
RESULT 1094
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A B B B B

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Score 109.2; DB 11; Length 128668; Pred. No. 2e-22;
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                            Length 51961
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Human digestive system antigen genomic sequence SEQ ID NO: 4741
WO200155314-A2.
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Human testicular antigen encoding DNA fragment SEQ ID NO: 3149.
WO200155317-A2.
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Human testicular antigen encoding DNA fragment SEQ ID NO: 3150.
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                                                                                                                                                                           ABZ67488 standard, DNA, 51961 BP.
Human secreted protein encoding genomic DNA SEQ ID NO 1011.
W200271186-A2.
03-CCT-2002.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAL05933 standard; DNA; 15514 BP.
Human reproductive system related antigen DNA SEQ ID NO:
WO200155320-A2.
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Human pancreatic cancer related genomic DNA, SEQ ID NO:
WO200155206-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.9%; Score 109.2; DB 10;
Best Local Similarity 78.9%; Pred. No. 1.2e-22;
Query Match 5.9%; Score 109.2; DB 10; Best Local Similarity 78.9%; Pred. No. 1.2e-22; RESULT 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.9%; Score 109; DB 13; 78.3%; Pred. No. 1.7e-23;
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117 Match 5.9%; Score 109; DB 4;

12 Local Similarity 79.9%; Pred. No. 5.4e-23;
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5.9%; Score 109; DB 4;
Similarity 76.7%; Pred. No. 6.5e-23;
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ry Match
5.9%; Score 109; DB 4;
t Local Similarity 76.7%; Pred. No. 6.5e-23;
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ry Match
t Local Similarity 76.7%; Pred. No. 6.5e-23;
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Query Match
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RESULT 1123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAK76168 standard; DNA; 25541 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30980.
WO200157182-A2.
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Human respiratory system associated polypeptide-related DNA SeqID797.
US2003077704-A1.
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US2003077704-A1.
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Genomic sequence #203 encoding for novel human respiratory antigen.
WO200155448-A1.
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Genomic sequence #208 encoding for novel human respiratory antigen.
W0200155448-A1.
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Human testicular antigen encoding DNA fragment SEQ ID NO: 3151
WO200155317-A2.
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(HUMA-) HUMAN GENOME SCI INC.
ery Match
5.9%; Score 109; DB 11; Length 32146;
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ry Match
5.9%; Score 109; DB 10; Length 32248;
t Local Similarity 79.9%; Pred. No. 1e-22;
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Human reproductive system related antigen DNA SEQ ID NO: 8623.
WO200155320-A2.
02-AUG-2001.
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Best Local Similarity 79.9%; Pred. No. 1e-22;
RESULT 1114
ID AD641564 standard; DNA; 32248 BP.
DE Human respiratory system associated genomic DNA seq id 802.
PN US2003215893-A1.
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5.9%; Score 109; DB 4;
it Local Similarity 76.7%; Pred. No. 6.5e-23;
                                                                                                      5.9%; Score 109; DB 4; 76.7%; Pred. No. 6.5e-23;
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ry Match
t Local Similarity 79.9%; Pred. No. 8.8e-23;
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(HUMA-) HUMAN GENOME SCI INC.
6ry Match 5.9%; Score 109; DB 4
ery Match 79.9%; Pred. No. 1e-22;
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(HUMA-) HUMAN GENOME SCI INC.
                                               02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
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(HUMA-) HUMAN GENOME SCI INC.
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...AA2.
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...AT MALCh
Best Local Similarity 7
RESULT 1110
ID AA228363 stand?
DE Genomic ser
PN WO2011:-
PD 02-**
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RESULT 1111
D ADG41559 stand*
DE Human resp*
PD 20.
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J-A2.

J-A2.

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J-A3.

J-A3.

J-A3.

J-A3.

J-A3.

RESULT 108

J-A3.

J-A3.

RESULT 1108

J-A3.

J-A3.

RESULT 1108

J-A3.

...A2.
...A. HUMAN GENON.
...ry Match
Best Local Similarity
RESULT 1107
ID AAL05335 stand-
DE Human reprr
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PP 02-*
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RESULT 1113
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Best Local Similarity
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Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23335.
W0200157182-A2.
O9-AUG-2001.
HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 79.2%; Pred. No. 1e-2;
                                                                                                             AAK76172 standard; DNA; 34435 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30984.
WO200157182-A2.
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(ISIS-) ISIS PHARM INC.
6ry Match 5.9%; Score 109; DB 13; Length 94001;
rry... anilarity 72.8%; Pred. No. 2e-22;
PD 24-APR-2003.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 5.9%; Score 109; DB 11; Length 32248;

Best Local Similarity 79.9%; Pred. No. 1e-22;

RESULT 1116
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                                                                                                                                                                                                                               Length 34435;
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Human DADI carcinoma associated gene, SEQ ID NO:1478.
WO2003057146-A2.
                                                                                                                                                                                                                                                                                                                          Human LAR related nucleotide sequence SEQ ID NO:20 WO2004010956-A2.
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PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

Querry Match 5.9%; Score 108.8; DB 6;

Best Local Similarity 79.2%; Pred. No. 2e-23;

RESULT 1120
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Query Match 5.9%; Score 108.8; DB 5;
Best Local Similarity 79.5%; Pred. No. 9.9e-24;
                                                                                                                                                                                09-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ETY MATCH 5-9%; Score 109; DB 4;
St Local Similarity 79.9%; Pred. No. 1.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABV46377 standard; cDNA; 556 BP.
Human prostate expression marker cDNA 46368.
WO200160860-A2.
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Human cDNA of the invention SEQ ID NO:2282.
EP1347046-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABA96807 standard; cDNA; 1777 BP. Human uteroglobin 9-encoding cDNA.WO200198337-A1.
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Human DAD1 gene.
WO2003008583-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADC85440 standard; DNA; 44325 BP.
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ID ADJ33491 standard; DNA; 94001 BP
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2003.
(SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 1118
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Human musculoskeletal system related polynucleotide SEQ ID NO 3620.
WO200155367-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human musculoskeletal system-associated genomic DNA - SEQ ID 3620.
US2004009488-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 108.6; DB 12; Length 110000; Pred. No. 2.9e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.9%; Score 108.6; DB 10; Length 167163; Best Local Similarity 77.0%; Pred. No. 3.7e-22;
                                                                                                                                                                                                                                                                                                                                                                           Length 127943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.9%; Score 108.6; DB 12; Length 25899; 80.2%; Pred. No. 1.2e-22;
                   Score 108.8; DB 10; Length 44325;
Pred. No. 1.4e-22;
                                                                                                                                                                                                        Query Match 5.9%; Score 108.8; DB 12; Length 44325; Best Local Similarity 76.1%; Pred. No. 1.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
ry Match
r Match
r Local Similarity 80.2%; Pred. No. 3.9e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 108.6; DB 8; Length 65464; Pred. No. 2.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABX60243 standard; cDNA; 4140 BP.
cDNA encoding novel human musculoskeletal system antigen #2587.
US2002147140-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-40G-2001.
(HUMA-) HUMAN GENOME SCI INC.
Ery Match
5.9%; Score 108.6; DB 4; Length 4140;
Trans Similarity 80.2%; Pred. No. 3.9e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.9%; Score 108.6; DB 8; Length 4140; 80.2%; Pred. No. 3.9e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADQ59374 standard; DNA; 25899 BP.
Human cancer-associated (CA) gene sequence SEQ ID NO:10.
WO2004058288-A1.
                                                                                                                                                                                                                                                                   ADQ97651 standard; DNA; 127943 BP.
Human cancer associated sequence HD10-021, SEQ ID 628.
WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABX13172 standard; DNA; 65464 BP.
Human gene encoding a Noelin-1-like secreted protein.
US2002173459-Al.
                                                                                                                                                                                                                                                                                                                     PD 22-JUJ-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 74.6%; Pred. No. 2.7e-22;
RESULT 1127
                                                                             ADM74555 standard; DNA; 44325 BP.
Human carcinoma associated (CA) nucleic acid #112.
US2004072154-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE82948 standard; DNA; 167163 BP.
Human PVT1 genomic DNA sequence.
WO2003080808-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ30993 standard; DNA; 4140 BP
                   5.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-2004.
(SAGR-) SAGRES DISCOVERY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-OCT-2003.
(SAGR-) SAGRES DISCOVERY.
Query Match 5.9
(SAGR-) SAGRES DISCOVERY.
                                                                                                                                        15-APR-2004.
(MORR/) MORRIS D W.
(ENGE/) ENGELHARD E K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
RESULT 1132
Query Match
Best Local Similarity
RESULT 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
ROSE/) RUBEN S M.
A (BARA/) BARASH S C.
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 1131
                 Query Match
Best Local Similarity
RESULT 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-NOV-2002.
(PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1128
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AAK67282 standard; DNA; 33147 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22094
AAD58742 standard; DNA; 20733 BP.
Human transmembrane serine protease (TSP1-TSP34) gene fragment #3.
WO2003064641-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-DEC_2003.
(ISIS-) ISIS PHARM INC.
ery Match 5.9%; Score 108.4; DB 12; Length 104245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.9%; Score 108.4; DB 12; Length 104245; 66.7%; Pred. No. 3.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S.9%; Score 108.4; DB 13; Length 107745; Local Similarity 78.2%; Pred. No. 3.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 39703;
                                                                                              Ouery Match

S.9%; Score 108.4; DB 9; Length 20733;

BESULT 1135

ID AAL04340 standard; DNA; 32194 BP.

DE Human reproductive system related antigen DNA SEQ ID NO: 7028.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match

S.9%; Score 108.4; DB 4; Length 32194;

Best Local Similarity 79.5%; Pred. No. 1.6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMAN GENOME SCI INC.
ry Match
t Local Similarity 77.9%; Pred. No. 1.6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Applises standard; DNA; 170245 BP.
Renal cell carcinoma differentially expressed gene #322.
W020048933-A2.
10-UTN-2004
(AMHP) WYETH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADG86768 standard; DNA; 104245 BP.
Human clone RP1-109F14 from chromosome 6p21.2-21.3.
US2003224514-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match
Best Local Similarity 76.4%; Pred. No. 1.86-22;
RESULT 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABD33242 standard; DNA; 107745 BP.
Human cancer-associated (CA) gene HD07-040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADL34706 standard; DNA; 104245 BP.
Human PPAR-delta DNA fragment SEQ ID 4.
US2004063129-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC86430 standard; DNA; 39703 BP.
Human GPCR gene SEQ ID NO:883.
EP1270724-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MO2004059146-A2.

15-UTL-2004.

(SAGR-) SAGRES DISCOVERY INC.

127 Match
                                                                               07-AUG-2003.
(GENE-) GENEPROT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity RESULT 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
RESULT 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-2004.
(GAAR/) GAARDE W.
(FREI/) FREIER S M
(WATT/) WATT A T.
                                                                                                                                                                                                                                                                                                                                                                                               WO200157182-A2.
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Andrew Color of the Color

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Query Match
Best Local Similarity
RESULT 1159
ID ABV16579 standard, cl
DE Human prostate expres
PN W0200160866-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PI
Query Match
Best Local Similarity
RESULT 1151
ID ADC86642 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                     5.9%; Score 108.4; DB 12; Length 170245; 66.7%; Pred. No. 4.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 300001;
                                                                                                                                                                                                                                                                             5.9%; Score 108.4; DB 10; Length 300000; 78.2%; Pred. No. 6.2e-22;
                                                                                                                                                                                                                                                                                                                                                    Human protein tyrosine phosphatase 11 gene sequence SEQ ID NO:33 WO2004041216-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-DEC-2003.

1 (ISIS-) ISIS PHARM INC.

5.9%; Score 108.2; DB 12; Length 28001;

Ouery Match 78.8%; Pred. No. 1.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-DEC-2003.
(ISIS-) ISIS PHARM INC.
Query Match 5.9%; Score 108.2; DB 12; Length 28001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 108.2; DB 12; Length 28001;
Pred. No. 1.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 12; Length 28001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 4850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABA17986 standard; DNA; 4850 BP.
Human nervous system related polynucleotide SEQ ID NO 10317.
WO200159063-A2.
                                                                                                                                                                                                                                                                                                                                                                                             PD 21-MAY-2004.

PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE.

PA (UNIV-) UNIVERSITAETSKLINIKUM FREIBURG.

Query Match 5.9%; Score 108.4; DB 12;

BEST Local Similarity 78.2%; Pred. No. 6.2e-22;

RESULT 1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HG-AUG-2001.

(HUMA-) HUMAN GENOME SCI INC.

Ery Match

S.9%; Score 108.2; DB 5;

Ery Match

74.4%; Pred. No. 5.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.9%; Score 108.2; DB 12
78.8%; Pred. No. 1.7e-22;
                                                                                                                                                    RESULT 1143
ID ADE86352 standard; DNA; 300000 BP.
DE Human PTPN11 genomic DNA sequence SEQ ID NO:33.
PN WO2003022422-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADI36730 standard; DNA; 28001 BP.
Genomic DNA sequence #2 encoding human KOX 1.
US2003232438-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADI36729 standard; DNA; 28001 BP.
Genomic DNA sequence #1 encoding human KOX 1.
US2003232438-A1.
                                                                                                                                                                                                                                   (MOUN) MOUNT SINAI SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADM93170 standard; cDNA; 28001 BP.
Human KOX-1 variant cDNA sequence
US2004087536-A1.
                                                                                                                                                                                                                                                                                                                                    AD014076 standard; DNA; 300001 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADM93169 standard; DNA; 28001 BP.
Human KOX-1 genomic sequence.
US2004087536-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACN44018 standard; DNA; 45814 BP.
Human genomic sequence hCG33132.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
                      떠겨
  TWINE N C.
BURCZYNSKI M E
TREPICCHIO W I
                                                        (DORN/) DORNER A.
(STOV/) STOVER J A.
(SLON/) SLONI D K.
                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity RESULT 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
RESULT 1148
                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DOBI/) DOBIE K W. (FREI/) FREIER S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DOBI/) DOBIE K W. (FREI/) FREIER S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-MAY-2004
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                                                                                                                     Query Match
                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                    (BURC/)
(TREP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1149
ID ADM93170
DE Human KC
PN US200406
PD 06-MAY-.
PA (DOBI/)
PA (FREI/)
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5.9%; Score 108; DB 4; Length 51469;

DB AAK6932 standard; DNA; 51469 BP.

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24134.

PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match

Best Local Similarity 78.2%; Pred. No. 2.86-22;

RESULT 1157

ID ADE24797 standard; DNA; 186510 BP.

DE Human endothelin-1, EDN1, gene

PN US2003143544-A1.

PD 31-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAK78813 standard; DNA; 51469 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33625.
                                                                                                                                                                                     Length 349881;
5.9%; Score 108.2; DB 11; Length 45814; 78.8%; Pred. No. 2.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 186510;
                                                                                                                                                                                                                                                                                                                                                   Length 32249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

QUETY Match 5.9%; Score 108; DB 5; Length 32249;

Best Local Similarity 83.5%; Pred. No. 2.1e-22;

RESULT 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 51469;
                                                                                                                                                                                                                                AA199368 standard; DNA; 32249 BP.
Human excretory related polynucleotide SEQ ID NO 1132.
WO200155313-A2.
                                                                                                                                                                                                                                                                                                    PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

QUELY MARCh

Best Local Similarity 83.5%; Pred. No. 2.1e-22;

RESULT 1153

ID AA163718 standard; DNA; 32249 BP.

PWANGA Kidney related polynucleotide SEQ ID NO 1033.
                                                                                                                              PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

Query Match 5.9%; Score 108.2; DB 10;

Best Local Similarity 75.8%; Pred. No. 7.9e-22;

RESULT 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
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Pred. No. 6.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune,...
WO200157182-A2.
WO200157182-A2.
(99-AUG-2001.
(HUMA.) HUMAN GENOME SCI INC.
5.9%; Score 108; DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 107.8; DB Pred. No. 2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human prostate expression marker cDNA 16570.
WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
SEQ ID NO:6026.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PREDICTIVE MEDICINE. INC.
                                          Human GPCR gene SEQ ID NO:1095.
EP1270724-A2.
02-DAN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEST. 10.00 Similarity 78.2%; Pred RESULT 1155

ID AAK70270 standard; DNA; 51469 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH00191 standard; cDNA; 534 BE Human cDNA clone (3'-primer) SF EP1074617-A2.
07-FEB-2001.
(HELL-) HELIX RES INST.
Duery Match
Sest Local Similarity 79.1%; P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 80.5%;
RESULT 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA; 537
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02-AUG-2001
(HUMA-) HUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAL51575 standard; DNA; 4272 BP.
Human nucleic acid-associated protein coding sequence - SEQ ID No 58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24042 WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAL35859 standard; DNA; 9439 BP.
Human musculoskeletal system related polynucleotide SEQ ID NO 2224.
WO200155367-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.9%; Score 107.8; DB 10; Length 3887; 71.1%; Pred. No. 6.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.9%; Score 107.8; DB 13; Length 647; 51.8%; Pred. No. 2.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1579;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Length 5335;
                                                                   5.9%; Score 107.8; DB 5; Length 537; 79.0%; Pred. No. 2e-23;
                                                                                                                                                                                                                                6; Length 546;
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                                                                                                                                                                                                                                                                                                                                                                        DB 5; Length 621;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel canine microarray-related DNA sequence SeqID4731
WO2004063324-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAI99373 standard; DNA; 9439 BP.
Human excretory related polynucleotide SEQ ID NO 1137.
WO200155313-A2.
                                                                                                                     ABN62103 standard; cDNA; 546 BP.
Human cancer related polynucleotide SEQ ID NO 2070.
WO200214500-A2.
21-PEB-2002.
                                                                                                                                                                                                                                                                              AAS90974 standard; cDNA; 621 BP.
DNA encoding novel human diagnostic protein #26778
WO20015567-A2.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 8;
                                                                                                                                                                                                                                                                                                                                                                      5.9%; Score 107.8; DB 5 74.7%; Pred. No. 2.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADD72114 standard; cDNA; 3887 BP..
Human endozepine-like protein NOV1a cDNA NOV1a.
US2003195149-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.9%; Score 107.8; DB 8 74.7%; Pred. No. 7.2e-23;
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s.9%; Score 107.8; DB 4
L Local Similarity 74.7%; Pred. No. 1.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.9%; Score 107.8; DB 4 79.1%; Pred. No. 8.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 107.8; DB / Pred. No. 3.9e-23
                                                                                                                                                                                                                              5.9%; Score 107.8; DB 81.2%; Pred. No. 2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cDNA sequence SEQ ID NO:18381.
EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH18351 standard; cDNA; 1579 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAK69230 standard; DNA; 5335 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                       ADQ53429 standard; DNA; 647
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(PPIZ ) PFIZER PROD INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HELI-) HELIX RES INST.
Lry Match
best Local Similarity
RESULT 1160
ID ABN62103 standar
DE Human cancer
PN WO200214°
PD 21-FFF
PA (F
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RESULT 1163
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Best Local Similarity
RESULT 1164
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Best Local Similarity
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RESULT 1166
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RESULT 1168
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ADJ08557 standard; DNA; 17397 BP.
Human cardiovascular system associated polypeptide-related DNA SeqID1945.
US2004005575-Al.
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Human musculoskeletal system-associated genomic DNA - SEQ ID 2224.
US2004009488-A1.
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(HUWA-) HUMAN GENOME SCI INC.
(ery Match timilarity 74.7%; Score 107.8; DB 10; Length 17397;
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Pred. No. 1.5e-22;
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5.9%; Score 107.8; DB 4; Length 19334;
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WO200155321-A2.
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                                                                                                                                                                                                                                              ABXS8847 standard; cDNA; 9439 BP.
cDNA encoding novel human musculoskeletal system antigen #1191.
US2002147140-A1.
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WO200155321-A2.
                                                                                                                                                                                     Length 9439;
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                       DB 4; Length 9439;
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US2003059908-A1.
                                                                                 AAI63723 standard; DNA; 9439 BP.
Human kidney related polynucleotide SEQ ID NO 1038
WO200155323-A2.
                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.

5.9%; Score 107.8; DB 5;

t Local Similarity 74.7%; Pred. No. 1.2e-22;
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Pred. No. 1.2e-22;
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(HUMA-) HUMAN GENOME SCI INC.
ery Match 5.9%; Score 107.8; DB 1:
ery Match 74.7%; Pred. No. 1.7e-22;
HUMAN GENOME SCI INC.
5.9%; Score 107.8; DB 4
Similarity 74.7%; Pred. No. 1.2e-22;
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5.9%; Score 107.8; DB 4
Similarity 74.7%; Pred. No. 1.7e-22;
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Human potassium channel transporter gene.
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(BEASA) BEASLEY E M.
(WEIM) WEI M.
(KETC) KETCHUM K A.
(DFRA/) DI FRANCESCO V.
                                      Best Local Similarity RESULT 1169
                                                                                                                                                                                                                                                                                                                           (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cocal Similarity
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(HUMA-) HUM
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                       Query Match
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WO200224747-A2.
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28004005575-A1.
08-JAN-2004.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                          Human cardiovascular system associated polypeptide-related DNA SeqID1943.
US2004005575-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADB16928 standard; DNA; 49939 BP.
Human DYXC1 DNA, chromosomal gene region nucleotides 100001-150000.
WO2003068814-A1.
                                                                                                                                    5.9%; Score 107.8; DB 10; Length 19334; 74.7%; Pred. No. 1.8e-22;
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(HUMA-) HUMAN GENOME SCI INC.
ery Match
5.9%; Score 107.8; DB 4; Length 19345;
..... Similarity 74.7%; Pred. No. 1.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.9%; Score 107.8; DB 9; Length 49939; 79.1%; Pred. No. 3.2e-22;
                                                                                                                                                                                                                                                                                                                                                                     Human cardiovascular system antigen genomic DNA SEQ ID No 1944 WO200155321-A2.
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DNA encoding endothelin converting enzyme 1 (ECE-1) #1.
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                                                      Human cardiovascular system related genomic DNA #703 US2003059908-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE47138 standard; DNA; 19345 BP.
Human cardiovascular system related genomic DNA #704.
US2003059908-A1.
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(HUMA-) HUMAN GENOME SCI INC.
Ery Match 5.9%; Score 107.8; DB 1(
                                                                                                                                                                                                                                                                                        5.9%; Score 107.8; DB 1 74.7%; Pred. No. 1.8e-22;
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Pred. No. 2.3e-22;
74.7%; Pred. No. 1.8e-22;
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Human genomic sequence hCG24994.
WO2003073826-A2.
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                                                                                                                                                                                              ADJ08555 standard; DNA; 19334 BP
                                                                                                                                                                                                                                                                                                                                                  AAS36444 standard; DNA; 19345 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADJ08556 standard; DNA; 19345 BP
                                      ADE47137 standard; DNA; 19334 BP
                                                                                          27-MAR-2003.
(HUMA-) HUMAN GENOME SCI INC.
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(HUMA-) HUMAN GENOME SCI INC.
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ry Match 5.9%;
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US2004110701-Al.
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(LICN ) LICENTIA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
RESULT 1181
ID ADJ08556 standard; DN
DE Human cardiovascular
PN USZO04005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME
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SULT 1185
                                                                                                                                                      Local Similarity
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Best Local Similarity
RESULT 1180
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RESULT 1186
ID ABK94411 standard; L
DE DNA encoding endothe
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
  Best Local Similarity
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Genomic sequence #169 encoding novel human connective tissue polypeptide. WO200155343-A1. 02-AUG-2001. (HUMA-) HUMAN GENOME SCI INC.
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Genomic sequence #204 encoding for novel human respiratory antigen.
WO200155448-Al.
                                                                                                                                                                                                                                                                                                       5.9%; Score 107.8; DB 13; Length 110000; 79.1%; Pred. No. 5.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 107.6; DB 11; Length 152330;
Pred. No. 7.4e-22;
                                                                                                                                                                                                                                   DB 12; Length 109906;
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A (CNRS) CNRS CENT NAT RECH SCI.
COURT MATCH
5.8%; Score 107.6; DB 5; Length 110000;
Best Local Similarity 80.1%; Pred. No. 6.1e-22;
                                       5.9%; Score 107.8; DB 6; Length 109906; 79.1%; Pred. No. 5.2e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 21470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.8%; Score 107.6; DB 4; Length 21470; 78.4%; Pred. No. 2.2e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL84412 standard; cDNA; 397 BP.
Human ovarian cancer related cDNA clone SEQ ID NO:7390.
WO200192581-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.8%; Score 107.6; DB 11;
80.1%; Pred. No. 5.8e-22;
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20-MAR-2003.

(HUMA.) HUMAN GENOME SCI INC.

5.8%; Score 107.6; DB 9;

sery Match

5.8%; Score 107.6; DB 9;

5.8%; Pred. No. 2.2e-22;
                                                                                                                                                                                                                                5.9%; Score 107.8; DB 1279.1%; Pred. No. 5.2e-22;
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Nucleotide sequence of the human SPG4 gene.
FR2798138-A1.
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Connective tissue related genomic DNA #169.
US2003054375-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cDNA of the invention SEQ ID NO:1678.
EP1347046-Al.
                                                   EBST Local Similarity 79.1%; Score 107.8; BEST Local Similarity 79.1%; Pred. No. 5.2 ID ADL08112 standard; DNA; 109906 BP.

EBSULT 1187

ID ADL08112 standard; DNA; 109906 BP.

EBSULT Human gene associated with low HDL-C ECEI.PN US2004043389-A1.
28-MAR-2002.
(EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1193
ID ACM45070 standard, DNA; 152330 BP.
DE Human genomic sequence hCG32392.
PN WO20003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                            DNA; 21470 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADM02993 standard; cDNA; 2553 BP
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Local Similarity 78.4%;
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(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                  04-MAR-2004.
(VITI-) VITIVITY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-DEC-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                    Best Local Similarity
RESULT 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1190
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Best Local Similarity
RESULT 1191
                                                                                                                                                                                                                                                                                                                                                                         ABK42270 standard;
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                                            Query Match
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5.8%; Score 107.2; DB 6; Length 1679; 68.9%; Pred. No. 6.3e-23;
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Human FLAP genomic DNA SEQ ID NO:1.
WO2004035741-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC86168 standard; DNA; 21704 BP. Human GPCR gene SEQ ID NO:621. EP1270724-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABQ77404 standard; DNA; 78025 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABS55783 standard; cDNA; 1621 BP
                                                                                                                                                                                      24-SEP-2003.
(REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-SEP-2004.
(SAGR-) SAGRES DISCOVERY INC.
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(VITI-) VITIVITY INC.
                                                                                   Best Local Similarity
RESULT 1206
ID ADMO2334 standard; CD
DE Human CDNA of the inv
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIO
                                                                                                                                                                                                                                         Best Local Similarity
RESULT 1207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human SELP DNA. WO2003016494-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JAN-2003.
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Best Local Si
RESULT 1212
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                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                               ADI97334 standard; DNA; 17498 BP.
Human respiratory system associated polypeptide-related DNA SeqID798.
US2003077704-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAK82098 standard; DNA; 46366 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36910.
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAK79437 standard; DNA; 708 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34249.
WO200157182-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.8%; Score 107.4; DB 12; Length 202100; 77.5%; Pred. No. 1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Uuery Match 5.8%; Score 107.4; DB 13; Length 87847; Best Local Similarity 69.2%; Pred. No. 6.1e-22; RESULT 1201
                                                                                                                                                                                                                                                                                                                                    24-APR-2003.
(HUMA-) HUMAN GENOME SCI INC.
(ery Match
(ery Match
5.8%; Score 107.4; DB 11; Length 17498;
                                                                                                                                                                                                                           5.8%; Score 107.4; DB 10; Length 17498; 79.4%; Pred. No. 2.3e-22;
                                                                    5.8%; Score 107.4; DB 4; Length 17498; 79.4%; Pred. No. 2.3e-22;
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ry Match
t Local Similarity 76.3%; Pred. No. 4.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.8%; Score 107.2; DB 5; Length 1504; 84.3%; Pred. No. 5.9e-23;
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(HUMA-) HUMAN GENOME SCI INC.
ery Match 5.8%; Score 107.2; DB 4; Length 708;
                                                                                                                     *ADG41560 standard; DNA; 17498 BP.
Human respiratory system associated genomic DNA seg id 798.
US2003215893-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAL51168 standard; cDNA; 1679 BP.
Peroxidase-related protein 12-21 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human IDE/ KNSL1 genomic sequence, SEQ ID 484. WO2003054143-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jr 1200
Ambū3066 standard; DNA; 87847 BP.
Mman cancer-associated genomic DNA HD23-013.
WO2004074320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human IDE/KNSL1 gene DNA sequence SeqID484 US2003224380-A1.
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10-APR-2002.
(BODE-) BODE GENE DEV CO LTD SHANGHAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NISC-) JAPAN SCI & TECHNOLOGY CORP.

Ouery Match
5.8%: Score 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADE43315 standard; DNA; 202100 BP
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                                                                                                                                                                                20-NOV-2003.
(HUMA-) HUMAN GENOME SCI INC.
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(SAGR-) SAGRES DISCOVERY INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-DEC-2003.
(GEHO ) GEN HOSPITAL CORP.
Best Local Similarity
RESULT 1197
ID ADG41560 standa
DB Human respi
PN US20037
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Best Local Similarity
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Best Local Similarity
RESULT 1203
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Best Local Similarity
RESULT 1199
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Best Local Similarity
RESULT 1202
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RESULT 1205
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AAK69092 standard; DNA; 9454 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23904.
WO200157182-A2.
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Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23905.
WO200157182-A2.
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PA (DECO-) DECODE GENETICS EHF.

Guery Match

Best Local Similarity 80.4%; Pred. No. 8.2e-22;

RESULT 12.13

ID ADS94372 standard; DNA; 398800 BP.

DE Human 5-lipoxygenase activating protein (FLAP) gene.

PN WO2004035746-A2.

PD 29-APR-2004.

PA (DECO-) DECODE GENETICS EHF.

S.8%; Score 107.2; DB 13; Length 110000;

Best Local Similarity 80.4%; Pred. No. 8.2e-22;
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Best Local Similarity 70.8%; Pred. No. 6.6e-22;
RESULT 1211
                                                                                                                                                       Length 2455;
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                                                                                                                                                                                                                                                                                                                    PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.8%; Score 107.2; DB 4; Length 9454;
Best Local Similarity 80.4%; Pred. No. 1.8e-22;
RESULT 1208
                                                                                                                                                    5.8%; Score 107.2; DB 11; 75.7%; Pred. No. 8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
EY MAtch
Local Similarity 77.1%; Pred. No. 3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.

ry Match
5.8%; Score 107.2; DB 4;
t Local Similarity 80.4%; Pred. No. 2.6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABD32761 standard; DNA; 103375 BP.
Human cancer-associated genomic DNA HD16-030.
WO2004074320-A2.
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ADM02334 standard; cDNA; 2455 BP.
Human cDNA of the invention SEQ ID NO:1019.
EP1347046-A1.
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(BODE-) BODE GENE DEV CO LTD SHANGHAI.
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Query Match
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                                                                                                                                                                                                                                                                                                                                                 ABK42490 standard; DNA; 7359 BP.
Genomic sequence #389 encoding novel human connective tissue polypeptide.
WO200155343-Al.
                                                                                                                                                                                                       ABK42489 standard; DNA; 7359 BP.
Genomic sequence #388 encoding novel human connective tissue polypeptide.
WO200155343-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23874.
WO200157182-A2.
09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK69061 standard; DNA; 7359 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23873.
WO200157182-A2.
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Human testicular antigen encoding DNA fragment SEQ ID NO: 2108.
WO200155317-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AALO4533 standard; DNA; 7625 BP.
Human reproductive system related antigen DNA SEQ ID NO: 7221.
WO20<u>01</u>55320-A2.
                                                                              Genomic sequence #330 encoding novel human enzyme polypeptide WO200155301-A2.
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(HUMA-) HUMAN GENOME SCI INC.
5.8%; Score 107; DB 4; Length 7625;
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       Length 1621;
                                                                                                                                                             Length 6437;
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     5.8%; Score 107; DB 6; 76.5%; Pred. No. 7.2e-23;
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02-AUGLOON.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
5.8%; Score 107; DB 4;
1ery Match
5.8%; Pred. No. 1.7e-22;
                                                                                                                                                                                                                                                                02-AUG-2010.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
5.8%; Score 107; DB 4;
ery Match 79.7%; Pred. No. 1.8e-22;
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ry Match

5.8%; Score 107; DB 4;

t Local Similarity 79.7%; Pred. No. 1.8e-22;
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ry Match 5.8%; Score 107; DB 4;
t Local Similarity 79.7%; Pred. No. 1.8e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB60646 standard; DNA; 7359 BP.
Connective tissue related genomic DNA #389.
US2003054375-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Connective tissue related genomic DNA #388 US2003054375-A1.
                                                               DNA; 6437 BP.
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(HUMA-) HUMAN GENOME SCI INC.
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(HUMA-) HUMAN GENOME SCI INC.
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Query Match 5.8%;
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J34375-A1.

AAR-2003.

(HUMA-) HUMAN GENOME

Query Match
Best Local Similarity 75.

RESULT 1221

ID ADB60645 standa~

DE Connective PR US20030° PP 20~

PP 20~

PA
Query Match
Best Local Similarity
RESULT 1215
ID AAS42014 standard; DN
DE Genomic sequence #330
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME
                                                                                                                                                                   Best Local Similarity
RESULT 1216
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
RESULT 1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
RESULT 1219
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RESULT 1223
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1220
ID ADB6064(
DE Connecti
PN US200300
PD 20-MAR-2
PA (HUMA-)
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ABL52838 standard; DNA; 39265 BP.
Polynucleotide sequence related to an analgesic peptide-like structure.
WO200204642-A1.
                                                                                                                                                                                                                                 AAK91264 standard; DNA; 28563 BP.
Human digestive system antigen genomic sequence SEQ ID NO: 4840.
WO200155314-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-003.
03-00L-2003.
(INCY-) INCYTE GENOMICS INC.
6ry Match 5.8%; Score 107; DB 10; Length 173805;
6ry Match 79.7%; Pred. No. 1.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 108316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 110000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 110000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 57013;
                                                                           Genomic sequence #31..., Genoding novel human enzyme polypeptide. WO200155301-A2. 02-AUG-2001. (HUMA-) HUMAN GENOME SCI INC. 5.8%; Score 107; DB 4; Length 9742; St Local Similarity 79.7%; Pred. No. 2.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 13; Length 51837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 39265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 485;
                                                                                                                                                                                                                                                                                                                                         Length 28563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADLI3775 standard; DNA; 173805 BP.
Osteoarthritis-associated polymorphic nucleotide #307.
WO2003054166-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 106.8; DB 6;
Pred. No. 4e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY. (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO. 
LY MALCH ES. 8%; Score 107; DB 10; 
tt Local Similarity 79.7%; Pred. No. 9.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 5.8%; Score 107; DB 11;
Local Similarity 79.7%; Pred. No. 6.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 107; DB 10;
Pred. No. 9.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                               PD 17-JAN-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
QUETY MATCH 5.8%; Score 107; DB 6;
Best Local Similarity 78.0%; Pred. No. 5.1e-22;
RESULT 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 107; DB 10;
Pred. No. 9.5e-22;
Best Local Similarity 78.0%; Pred. No. 1.9e-22;
RESULT 1224
                                                                                                                                                                                                                                                                                        02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
6ry Match
ery Match
6ry Match 78.0%; Pred. No. 4.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAGRE) SAGRES DISCOVERY INC.
(SAGR.) SAGRES DISCOVERY INC.
5.8%; Score 107; DB 13
cimilarity 78.0%; Pred. No. 6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABD33453 standard; DNA; 51837 BP.
Human cancer-associated (CA) gene HD07-086.
WO2004058146-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene #420 used to diagnose liver cancer.
WO200229103-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC87336 standard, DNA, 108316 BP. Human GPCR gene SEQ ID NO:1789. EP1270724-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACN45046 standard; DNA; 57013 BP. Human genomic sequence hCG39345. WO2003073826-A2.
                                                             AAS42015 standard; DNA; 9742 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABN93922 standard; DNA; 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
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                                                                                                                                                                                   Best Local Similarity RESULT 1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
RESULT 1234
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
RESULT 1226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1232
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vuery Match 5.8%; Score 106.8; DB 11; Length 8250;
Best Local Similarity 75.9%; Pred. No. 2.3e-22;
RESULT 1240
                                                                                                                                                                                                                                                                                                                                                                                       Match 5.8%; Score 106.8; DB 12; Length 8250; Local Similarity 75.9%; Pred. No. 2.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 5.8%; Score 106.8; DB 11; Length 8270; Local Similarity 75.9%; Pred. No. 2.3e-22;
                                                                                                  Query Match 5.8%; Score 106.8; DB 6; Length 8250; Best Local Similarity 75.9%; Pred. No. 2.3e-22; RESULT 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.8%; Score 106.8; DB 6; Length 8270; 75.9%; Pred. No. 2.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADP68285 standard, DNA, 8270 BP.
Human NOV14a DNA encoding a B7-H2 like protein SeqID 47
WO200281510-A2.
                                                                                                                                                 ADP68256 standard; DNA; 8250 BP.
Human NOV3b DNA encoding a B7-H2 like protein SeqID 17.
WO200281510-A2.
                                                                                                                                                                                                                                                                                                 ADH71873 standard; DNA; 8250 BP.
Human gene of the invention NOV31a SEQ ID NO:769.
WO2003102155-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADM47750 standard; DNA; 8270 BP.
NOV14 coding sequence, SEQ ID 47.
WO200268647-A2.
                  ADH47720 standard; DNA; 8250 BP. NOV3b coding sequence, SEQ ID 17. WO200268647-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1243
ID ADL25633 standard; DNA; 8270 BP.
DE Human diagnostic gene, NOV14.
PN US2004005557-Al.
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PENA C B A.
TCHERNEV V T.
ZERHUSEN B D.
MILLET I.
MILLET G E.
LEPLEY D M.
SMITHSON G.
                                                                       06-SEP-2002.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                             17-OCT-2002.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-OCT-2002.
(CURA-) CURAGEN CORP.
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SPYTEK K A.
BOLDOG F L.
VERNET C A M.
                                                                                                                                                                                                                                                                                                                                                                        (CURA-) CURAGEN CORP.
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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EDINGER S R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHENOY S G.
CASMAN S J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PADIGARU M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MALYANKAR
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     RESULT 1238
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                                                                                                                                                                                                                                                                                                                                                                                                         AAK67814 standard; DNA; 5289 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22626.
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 106.8; DB 12; Length 8249;
Pred. No. 2.3e-22;
                                               22-0CT-1998.
(GEMY) GENETICS INST INC.
6TW Match 5.8%; Score 106.8; DB 2; Length 2754;
ery Match 79.0%; Pred. No. 1.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        OS-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ELY Match 5.8%; Score 106.8; DB 4; Length 5289;
ery Match 5289;
-- ' A Similarity 79.0%; Pred. No. 1.7e-22;
                                                                                                                                                                                                                                                                                                                                                        DB 6; Length 2754;
                                                                                                                                                                                                                                                                                                                                                      5.8%; Score 106.8; DB 679.0%; Pred. No. 1.2e-22;
AAV62746 standard; cDNA; 2754 BP.
Human secreted protein clone en539_8 cDNA.
WO9846757-A2.
                                                                                                                                      ABQ92049 standard; cDNA; 2754 BP. Human polynucleotide SEQ ID NO 46. USC002065394-A1. 30-MX*-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADL25603 standard; DNA; 8249 BP. Human diagnostic gene, NOV3b.
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                                                                                                                                                                                                      JACOBS K.
MCCOY J M.
LAVALLIE E R.
COLLINS-RACIE L A.
EVANS C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZERHIGEN B D.
MILLET I.
MILLET C E.
LEPLEY D M.
SMITHSON G.
BAUMGARINER J C.
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(ROTH/) ROTHENBERG M.
(STON/) STONE D J.
(BURG/) BURGESS C E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COLMAN S D.
SPYTEK K A.
BOLDOG F L.
VERNET C A M.
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PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HERRMANN J L.
                                                                                                                                                                                                                                                                                               (MERB/) MERBERG D.
(TREA/) TREACY M.
(SPAU/) SPAULDING V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GUO X.
EDINGER S R.
MACDOUGALL J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHERNEV V T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHIMKETS R A.
                                                                                     Ouery Match
Best Local Similarity
RESULT 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LI L.
SHENOY S G.
CASMAN S J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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GORMAN L.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEZES P D.
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                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                            (MCCO/)
(LAVA/)
(COLL/)
(EVAN/)
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1236
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WO2003054143-A2.
                                                                                                                                                                                                                                   Human musculoskeletal system related polynucleotide SEQ ID NO 3236.
WO200155367-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADJ30609 standard; DNA; 15745 BP.
Human musculoskeletal system-associated genomic DNA - SEQ ID 3236.
US2004009488-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PD 15-JAN-2004.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match

5.8%; Score 106.8; DB 12; Length 15745;

Best Local Similarity 79.0%; Pred. No. 3.4e-22;

RESULT 1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.8%; Score 106.8; DB 13; Length 63045; 82.6%; Pred. No. 7.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 63824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 12; Length 20000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 29360;
                                                                                                                                                                                                                                                                       02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ery Match 5.8%; Score 106.8; DB 4; Length 15745;
                                                                                                                                                            5.8%; Score 106.8; DB 12; Length 8270; 75.9%; Pred. No. 2.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.8%; Score 106.8; DB 8; Length 15745; 79.0%; Pred. No. 3.4e-22;
                                                                                                                                                                                                                                                                                                                                                                         ABX59859 standard; cDNA; 15745 BP. cDNA encoding novel human musculoskeletal system antigen #2203.
US2002147140-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A truncated portion of DNA encoding human kinesin-like 1. US2004180847-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADQ97189 standard; DNA; 29360 BP.
Human cancer associated sequence HD08-012, SEQ ID 165.
WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE43743 standard; DNA; 63824 BP.
Polymorphic human KNSL1 genomic sequence, SEQ ID 348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 106.8; DB 10;
Pred. No. 7.9e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WOLVELL
22-JULI-2004.
(SACH-) SAGRES DISCOVERY INC.
5.8%; Score 106.8; DB 12
5.8%; Pred. No. 4.9e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.8%; Score 106.8; DB 1.75.9%; Pred. No. 3.9e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 82.6%; Pred. No. 7.
REGULT 1250
ID AD843742 standard; DNA; 63824 BP.
DE Human KNSL1 genomic sequence, SEQ ID 347.
PN WO2003054443-A2.
PD 03-JUL-2003.
PA (SENP.) NEUROGENETICS INC.
PA (GEHO ) GEN HOSPITAI. CODD
                                                                                                                                                                                                                   AAL36871 standard; DNA; 15745 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADN58769 standard; DNA; 20000 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADR72312 standard; DNA; 63045 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human B7H DNA #4.
US2004102398-A1.
27-MAY-2004.
(ISIS-) ISIS PHARM INC.
(TAUP/) TAUPIER R J.
(GERL) GERLACH V.
(GROS/) GROSSE W M.
(LIUX/) LIU X.
(ELLE/) ELLERMAN K.
(ROTH) ROTHENBERG M.
(STOM/) STONE D J.
(STOM/) BURGESS C E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -98-A1.
-2004.
-AT MATCH
BEST LOCAL SIMILARITY
RESULT 1248
ID ADQ91189 stand*
DB Human cancr
PN W02004*
PD 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                10-OCT-2002.
(ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
RESULT 1245
                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
RESULT 1251
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Best Local Similarity
RESULT 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-SEP-2004.
(DOBI/) DOBIE K W.
(KOLL/) KOLLER E.
                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                  RESULT 1244
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5.8%; Score 106.8; DB 10; Length 202100; 82.6%; Pred. No. 1.6e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 110000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 110000;
                                             5.8%; Score 106.8; DB 10; Length 63824; 82.6%; Pred. No. 7.9e-22;
                                                                                                                                                                                                                                                                                PD 04-DEC-2003.

PA (GEHO) GEN HOSPITAL CORP.

Query Match 5.8%; Score 106.8; DB 12; Length 63824;

Best Local Similarity 82.6%; Pred. No. 7.9e-22;

RESULT 1254
                                                                                                                                                                              Score 106.8; DB 12; Length 63824; Pred. No. 7.9e-22;
                                                                                                                                                                                                                                                                                                                                                                                                   Est Local Similarity 67.1%; Pred. No. 9.8e-22; RESULT 1255

DE Human ACM44790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 98546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

ery Match

1.8*; Score 106.8; DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 106.8; DB 11;
Pred. No. 1.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.8%; Score 106.8; DB 11; 75.9%; Pred. No. 1.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 106.8; DB 11;
Pred. No. 1e-21;
                                                                                                                                                                                                                             ADH54221 standard; DNA; 63824 BP.
Human KNSL1 gene variant DNA sequence SeqID348.
US2003224380-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE43315 standard; DNA; 202100 BP. Human IDE/ KNSL1 genomic sequence, SEQ ID 484. 03-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABV50808 standard; cDNA; 426 BP.
Human prostate expression marker cDNA 50799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADH54357 standard; DNA; 202100 BP.
Human IDE/KNSL1 gene DNA sequence SeqID484.
US2003224380-A1.
                                                                                                                                                                                                                                                                                                                                                              Alici326 standard; DNA; 91000 BP.
Human farnesoid X receptor (FXR) DNA #2.
30-MAY-2003.
(ISIS-) ISIS PHARM INC.
                                                                                            ADH54220 standard; DNA; 63824 BP.
Human KNSL1 gene DNA sequence SeqID347.
US2003224380-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 1260
DDC86340 standard; DNA; 349901 BP.
Human GPCR gene SEQ ID NO:1393.
BP1270724-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACN44790 standard; DNA; 98546 BP.
Human genomic sequence hCG23145.
WO2003073826-A2.
                                                                                                                                    USZOCZZO
04-DEC-2003.
(GEHO ) GEN HOSPITAL CORP.
(GEHO ) GEN HOSPITAL S.8%;
lery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WOZOCZ
12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
Herv Match 5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NEUR-) NEUROGENETICS INC. (GEHO ) GEN HOSPITAL CORP.
03-JUL-2003.
(NEUR-) NEUROGENETICS INC.
(GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
RESULT 1259
                                                       Best Local Similarity
RESULT 1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 1261
                                                                                                                                                                                            Best Local Similarity RESULT 1253
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RESULT 1256
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RESULT 1258
                                               Query Match
                                                                                                                                                                                Query Match
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08-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADRO7572 standard; cDNA; 4095 BP.
Full length human cDNA useful for treating neurological disease Seq 1078.
EP1447413-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK42366 standard; DNA; 1382 BP.
Genomic sequence #265 encoding novel human connective tissue polypeptide.
WO200155343-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAK81284 standard; DNA; 442 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38096.
WO200157182-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.8%; Score 106.6; DB 12; Length 1754; Best Local Similarity 78.0%; Pred. No. 1e-22; RESULT 1265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.8%; Score 106.6; DB 13; Length 4095; 75.3%; Pred. No. 1.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 71.6%; Pred. No. 1.4e-22;
RESULT 1266
DE Full length human CDNA useful for treating neurological disease
PD BAUG-2004.
PD REAG-3 ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.8%; Score 106.6; DB 4; Length 1754; Best Local Similarity 78.0%; Pred. No. 1e-22; RESULT 1264
                                                                                                                                                                                                                         Query Match
5.8%; Score 106.6; DB 4; Length 553;
Beet Local Similarity 71.6%; Pred. No. 5e-23;
RESULT 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.8%; Score 106.4; DB 4; Length 442;
Best Local Similarity 70.1%; Pred. No. 5.1e-23;
                                                            Length 426;
               23-AUG-2001.
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
ery Match
5.8%; Score 106.6; DB 5;
or Incal Similarity 76.8%; Pred. No. 4.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.8%; Score 106.6; DB 8;
80.0%; Pred. No. 1.6e-21;
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                                                                                                       Human cDNA clone (3'-primer) SEQ ID NO:10067.
                                                                                                                                                                                                                                                                                                 AAK94142 standard; cDNA; 1754 BP.
Human full-length cDNA, SEQ ID NO: 2652.
EP1130094-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADL30619 standard; cDNA; 1754 BP.
Full length human cDNA clone SeqID 2652.
EP1396543-A2.
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Human BCR DNA corresponding to U07000.
DE10127572-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH16642 standard, CDNA, 3112 BP.
Human CDNA sequence SEQ ID NO:15764.
EP1074617-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAR-2004.
(REAS-) RES ASSOC BIOTECHNOLOGY.
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                05-SEP-2001.
(HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-FEB-2001.
(HELI-) HELIX RES INST.
                                                                                                                                                                                            07-FEB-2001.
(HELI-) HELIX RES INST.
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                                                                          Best Local Similarity
RESULT 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 1267
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WO200160860-A2.
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                                                              Query Match
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AAF97846 standard; DNA; 51474 BP.
Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:60.
WO200116311-A1.
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DNA encoding novel signal transduction pathway protein, Seq ID 1347.
WO200154733-A1.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 81.7%; Pred. No. 1.6e-21; Best Local Similarity 81.7%; Pred. No. 1.6e-21; Best Local Similarity 81.7%; Pred. No. 1.6e-21; DARS-2004 CP-22; PARS-2004 CP-22; Pred. No. 1.6e-21; Pred. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-AUG-2001.
(HUWA-) HUMAN GENOME SCI INC.
ery Match 5.8%; Score 106.4; DB 4; Length 24757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.8%; Score 106.4; DB 10; Length 24757; 83.0%; Pred. No. 6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 128978;
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PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
5.8%; Score 106.4; DB 4; Length 1382;
Best Local Similarity 79.6%; Pred. No. 1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABK83459 standard; cDNA; 128978 BP.

Human cDNA differentially expressed in granulocytic cells #30.
W0200228999-A2.

I.-ARP-2002.

(GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS33481 standard; DNA; 24757 BP.
DNA encoding human secreted protein, Seq ID No 764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 5.8%; Score 106.4; DB 12;
Local Similarity 79.3%; Pred. No. 1.4e-22;
                                                                                                                                                                                                                ADB60522 standard; DNA; 1382 BP.
Connective tissue related genomic DNA #265.
US2003054375-A1.
US2003054375-A1.
(HUMA-) HUMAN GENOME SCI INC.
STR. Score 106.4; DB 9;
EL LOCAL Similarity 79.6%; Pred. No. 1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.8%; Score 106.4; DB 6; Best Local Similarity 81.7%; Pred. No. 1.6e-21; RESULT 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A (HISM ) HISAMITSU PHARM CO LTD.
(GHIB-) CHIBA PREFECTURE.
OQUEYY MACLO Similarity 83.5%; Pred. No. 9.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.8%; Score 106.4; DB 83.0%; Pred. No. 6e-22;
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Human LIM kinase (LIMK) DNA #6.
WO200299048-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB94490 standard; DNA; 24757 BP. Novel human protein DNA #99. US2002168711-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADQ641085 standard; cDNA; 2419 BP.
Novel human cDNA sequence #1246.
EP1440981-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REAS-) RES ASSOC BIOTECHNOLOGY.
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(EXEL-) EXELIXIS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-NOV-2002.
(ROSE/) ROSEN C A..
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 1274
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RESULT 1276
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vuery Match 5.8%; Score 106.2; DB 12; Length 26865;
Best Local Similarity 78.6%; Pred. No. 7.3e-22;
RESULT 1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC61681 standard; DNA; 39796 BP.
Nucleotide sequence of the human ataxia gene.
WO200058461-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABD33616 standard; DNA; 122656 BP.
Human cancer-associated (CA) gene HD07-125.
WO2004058146-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACN43878 standard; DNA; 39148 BP.
Human genomic sequence hCG36720.
WO2003073826-A2.
                                                                                                   AAS36709 standard; DNA; 32190 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
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(SAGR-) SAGRES DISCOVERY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SAGR-) SAGRES DISCOVERY.
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RESULT 1292
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RESULT 1293
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RESULT 1296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADB83225 standard; cDNA; 688 BP.
Human cDNA sequence useful for the treatment of cancer (SeqID 1438)
WO2003050236-A2.
                                                                                                                                                                                                                                           DB 13; Length 128978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SAGR.) SAGRES DISCOVERY INC.
Query Match
S.8%; Score 106.4; DB 13; Length 243390;
Best Local Similarity 71.1%; Pred. No. 2.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 167932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Length 163350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACC46314 standard; cDNA; 3077 BP.
Human dithp zinc finger transcriptional regulator-encoding cDNA
WO200297031-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACC46358 standard; cDNA; 3084 BP.
Human dithp zinc finger transcriptional regulator-encoding cDNA
WO200297031-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 8658;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 688;
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Prostate and breast cancer associated human gene CYP17.
W02004028346-A2.
8-ARR-2004.
(AMSH ) AMERSHAM BIOSCIENCES SV CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AULI3501 standard; DNA; 167932 BP.
Osteoarthriis-associated polymorphic nucleotide #33.
WO2003054166-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G3-JUL-2003.

(INCY-) INCYTE GENOMICS INC.

5.8%; Score 106.4; DB 10;

ery Match

5.8%; Score 106.4; DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.8%; Score 106.2; DB 8; Beet Local Similarity 74.2%; Pred. No. 1.9e-22; RESULT 1285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.8%; Score 106.2; DB 9; 82.2%; Pred. No. 7.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 8;
                                                                                                                                                                                                                                     5.8%; Score 106.4; DB 13
81.7%; Pred. No. 1.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.8%; Score 106.4; DB 677.7%; Pred. No. 1.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.8%; Score 106.2; DB 8 74.2%; Pred. No. 1.9e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABD33366 standard; DNA; 243390 BP.
Human cancer-associated (CA) gene HD07-067.
WO2004058146-A2.
15-JUL-2004.
                        Drug therapy altered expressed gene #345.
WO2004072265-A2.
26-AUG-2004.
                                                                                                                                                                                                                                                                                                                        AAD46127 standard; DNA; 163350 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK69231 standard; DNA; 8658 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                 Human tumour suppressor gene. WO200268468-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1NCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                              (DORN/) DORNER A J. (TREP/) TREPICCHIO W L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Juliano Julian
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                                                                                                   (AMHP) WYETH.
(BURC/) BURCZYNSKI M.
(TWIN/) TWINE N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHIR) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 1283
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Best Local Similarity
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Best Local Similarity
RESULT 1287
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(PEKE ) PE CORP NY.
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Best Local Similarity
RESULT 1281
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ADJ08821 standard; DNA; 32190 BP.
Human cardiovascular system associated polypeptide-related DNA SeqID2209.
US2004005575-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1291
ID AAK78275 standard; DNA; 35959 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33087.
PN WO200157182-A2.
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(SAGR-) SAGRES DISCOVERY INC.
5.8%; Score 106.2; DB 13; Length 122656;
                                                                                                                                                                                                                                                       PD 27-MAR-2003.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match

5.8%; Score 106.2; DB 10; Length 32190;
Best Local Similarity 75.6%; Pred. No. 8.1e-22;
RESULT 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 106.2; DB 11; Length 39148; Pred. No. 9.1e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.8%; Score 106.2; DB 4; Length 35959; 78.6%; Pred. No. 8.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 39796;
Human cardiovascular system antigen genomic DNA SEQ ID No 2209.
WO200155321-A2.
02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                      Length 32190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     704
                                                                                                                                                                           ADE47403 standard; DNA; 32190 BP.
Human cardiovascular system related genomic DNA #969.
US2003059908-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABD33414 standard; DNA; 39983 BP.

Human cancer-associated (CA) gene HD07-077.

W W02004058146-A2.

15-JUL-2004.

CAGAR-) SAGRES DISCOVERY INC.

Guery Match

Best Local Similarity 74.2%; Pred. No. 9.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB-JAN-2004.

(HUMA-) HUMAN GENOME SCI INC.

5.8%; Score 106.2; DB 13;

ery Match

5.6%; Pred. No. 8.1e-22;
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Human cancer associated sequence HD10-034, SEQ ID
WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PA (RAPP) RAPPOLD-HOERBRAND G.
Query Match
Best Local Similarity 78.6%; Pred. No. 9.2e-22;
RESULT 1294
                                                                               vuery Match 5.8%; Score 106.2; DB 4; Best Local Similarity 75.6%; Pred. No. 8.1e-22; RESULT 1289
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Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22051.
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Human autoimmune disease-related genomic DNA sequence - SEQ ID 1706.
WO2004083403-A2.
                                                                                                                                                                                                                                                                                                                                                                   Human musculoskeletal system-associated genomic DNA - SEQ ID 2322. US2004009488-A1.
                                                                                                                                           ABXS8945 standard; cDNA; 16106 BP. cDNA encoding novel human musculoskeletal system antigen #1289. US2002147140-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABK83573 standard; cDNA; 130263 BP.
Human cDNA differentially expressed in granulocytic cells #144.
WO200228999-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.APR-2002.
(GENE-) GENE LOGIC INC.
(GENE-) GENE LOGIC INC.
5.8%; Score 106; DB 6; Length 130263;
Triniarity 79.6%; Pred. No. 2.2e-21;
                                                                                Score 106; DB 4; Length 16106;
Pred. No. 6.2e-22;
                                                                                                                                                                                                                                                                                           Length 16106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADS36465 standard; DNA; 25322 BP.
Human autoimmune disease-related genomic DNA sequence
WO2004083403-A2.
30-SEP-2004.
(APPL-) APPLERA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.8%; Score 106; DB 13; 79.6%; Pred. No. 9.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 106; DB 12;
Pred. No. 1.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                   15-JAN-2004.
(HUMA-) HUMAN GENOME SCI INC.
PY MATCH 5-8*; Score 106; DB 12;
st Local Similarity 79.6*; Pred. No. 6.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 106; DB 13;
Pred. No. 8.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 106; DB 10;
Pred. No. 1.8e-21;
                                                                                                                                                                                                                                                                                         5.8%; Score 106; DB 8; 79.6%; Pred. No. 6.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PD 09-AUG-2001.

PA (HDVA-) HUMAN GENOME SCI INC.

Query Match 5.8%; Score 106; DB 4;

Best Local Similarity 77.9%; Pred. No. 9.1e-22;

RESULT 1309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.8%; Score 106; DB 8; 73.7%; Pred. No. 1.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADJ53477 standard; DNA; 70000 BP.
Human PPP3CB genomic DNA #3.
US2004023382-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACH01384 standard; DNA; 96898 BP.
Human BIVM gene.
WO2003089595-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABQ77243 standard; DNA; 57130 BP.
Human MARK DNA.
                                                                                                                                                                                                                                                                                                                                                        DNA; 16106 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAK67239 standard; DNA; 30393 BP.
                                                                                5.8%;
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30-OCT-2003.
(UYSF-) UNIV SOUTH FLORIDA.
ELY MAtch...
5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-FEB-2004.
(ISTS-) ISIS PHARM INC.
Ouery Match
Best Local Similarity 77.9%;
Luery Match
Beet Local Similarity ''
RESULT 1305
ID ARXSB945 standar''
DE CDNA encodino
PN US20021471'
PA (ROST
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(APPL-) APPLERA CORP.
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 1306
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RESULT 1308
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RESULT 1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 1313
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                                                                                                                                                                                                                                                                                                                                                    ADJ29695 standard;
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Human retinal pigment epithelial-derived factor (PEDF) genomic DNA #3.
US2003096750-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK67366 standard; DNA; 16106 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAL35957 standard; DNA; 16106 BP.
Human musculoskeletal system related polynucleotide SEQ ID NO 2322.
WO200155367-A1.
                                                                                                                                                                                                                          5.8%; Score 106.2; DB 12; Length 137000; 70.9%; Pred. No. 2e-21;
                                                                                                                                                                                                                                                                                                                                                                                             5.8%; Score 106.2; DB 13; Length 161531; 78.6%; Pred. No. 2.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 349901;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABS57269 standard; DNA; 4421 BP.
Partial sequence #3 of genomic DNA encoding human PEDF
US6451763-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

Query Match
5.8%; Score 106.2; DB 10;

Best Local Similarity 78.6%; Pred. No. 3.5e-21;

RESULT 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 106; DB 10;
Pred. No. 2.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.8%; Score 106; DB 10; 70.2%; Pred. No. 2.8e-22;
                                                                              70.9%; Pred. No. 1.8e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.8%; Score 106; DB 9; 77.6%; Pred. No. 7.9e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.8%; Score 106; DB 4; 79.6%; Pred. No. 6.2e-22;
                                                                                                                                                                                                                                                                                    ABD33232 standard; DNA; 161531 BP.
Human cancer-associated (CA) gene HD07-038.
WO2004058146-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-SEP-2002.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC86940 standard; DNA; 349901 BP.
Human GPCR gene SEQ ID NO:1393.
EP1270724-A2.
                                                                                                                   ADH77370 standard; DNA; 137000 BP. Human PTPN12 polynucleotide #1. US2003232434-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACH39496 standard; cDNA; 562 BP.
Human foetal brain cDNA #863.
US2003073623-A1.
                                                                                                                                                                                                                                                                                                                                                 15-JUL-2004.
(SAGR-) SAGRES DISCOVERY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DRWA) DRWANAC R T.
(LABA/) LABAT I.
(STAC/) STACHE-CRAIN B.
(DICK/) DICKSON M C.
(JONE/) JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TOMB/) TOMBRAN-TINK J. (STEEL) F. R. (CHAD/) CHADER G J. (BECE,) BECERRA S P. (JOHN/) JOHNSON L V. (RODR/) ROBRIGUEZ I R.
                                                                                                                                                                                                      (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
RESULT 1304
ID AAL35957 standard; DN
DE Human musculoskeletal
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME
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Best Local Similarity
RESULT 1302
                                                                                                                                                                                                                     Query Match
Best Local Similarity
RESULT 1298
                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity
RESULT 1299
                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157182-A2.
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Length 96898;

Length 70000;

BBBBB

Length 34059

Length 57130;

Length 30393;

- SEQ ID 1679

Length 16106

Length 25322;

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RESULT 1323
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(ISIS-) ISIS PHARM INC.

5.7%; Score 105.8; DB 12; Length 19300;

Cuery Match

5.7%; Pred. No. 8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 105.8; DB 11; Length 99886; Pred. No. 2.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.7%; Score 105.8; DB 11; Length 31397; 78.9%; Pred. No. 1.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK84639 standard; cDNA; 9457 BP.
Human cDNA differentially expressed in granulocytic cells #1210.
WO200228999-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-AFF. 2002.
(GENE-) GENE LOGIC INC.
5.7%; Score 105.8; DB 6; Length 9457;
F Tocal Similarity 78.9%; Pred. No. 5.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2823;
                                                                                                                             Length 218336;
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                                                                                                                                                                                                                                                                                                                   Length 529;
                 ABQ76678 standard; DNA; 218336 BP.
Androgen receptor signalling pathway-associated DNA AF067844.
WQ200282081-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABA20423 standard; DNA; 2569 BP.
Human nervous system related polynucleotide SEQ ID NO 12754.
WO200159063-A2.
                                                                                                                                                                                                                                                                                                                   5.7%; Score 105.8; DB 6;
80.6%; Pred. No. 8.9e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.7%; Score 105.8; DB 5; 77.6%; Pred. No. 2.5e-22;
                                                                                                                                                                                  ABN60296 standard; cDNA; 529 BP.

Human cancer related polynucleotide SEQ ID NO 263
W0200214500-A2.
21-FEB-2002.
(CHIR ) CHIRON CORP.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                        MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

5.7%; Score 105.8; DB 5;

1.70-21 Similarity 70.9%; Pred. No. 9.4e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMAN GENOME SCI INC.

ry Match

t. Local Similarity 82.9%; Pred. No. 2.3e-22;
                                                                                                            vuery Match 5.8%; Score 106; DB 8;
Best Local Similarity 76.4%; Pred. No. 3e-21;
RESULT 1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adicsolv standard; cDNA; 2823 BP.

Human zinc finger protein 15 coding sequence.
W0200186890-Al.

(SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADP74371 standard; DNA; 19300 BP.
Human X chromosome nucleotides 469701-489000.
US2004110156-A1.
                                                                                                                                                                                                                                                                                                                                                                                                    Human prostate expression marker cDNA 54120.
WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACN44346 standard; DNA; 31397 BP.
Human genomic sequence hCG33404.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1322
ID ACN44066 standard; DNA; 99886 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genomic sequence hCG15674.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                              ABV54129 standard; cDNA; 585 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 80.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SAGR-) SAGRES DISCOVERY.
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(SAGR-) SAGRES DISCOVERY.
                                                                               17-OCT-2002.
(UYRP ) UNIV ROCHESTER.
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2001.
2001.
2NAI.
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Best Local Similarity
RESULT 1318
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Best Local Similarity
RESULT 1317
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                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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Best Local S
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RESULT 1314
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PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY.

Query Match
5.7%; Score 105.8; DB 11; Length 133632;
Best Local Similarity 82.5%; Pred. No. 2.6e-21;
RESULT 1326
ID AD019501 standard; DNA; 135005 BP.
DE Human soft Lissue sarcoma-upregulated DNA - SEQ ID 2320.
PN WO20040408938-A2.
PD 10-JUN-2004
PA (PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uuery Match 5.7%; Score 105.8; DB 12; Length 135005;
Best Local Similarity 75.8%; Pred. No. 2.6e-21;
RESULT 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 5.7%; Score 105.8; DB 13; Length 136284; Best Local Similarity 82.5%; Pred. No. 2.6e-21;
                                                                                                                            Length 101685;
                                                                                                                                                                                              Length 110000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-APR-2002.
(GENE-) GENE LOGIC INC.
(STY Match 5.7%; Score 105.8; DB 6; Length 136284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK83575 standard; cDNA; 136284 BP.
Human cDNA differentially expressed in granulocytic cells #146.
WO200228999-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.7%; Score 105.6; DB 4; Length 430; 72.6%; Pred. No. 9.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.7%; Score 105.6; DB 3; Length 438; 68.6%; Pred. No. 9.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.7%; Score 105.6; DB 6; Length 531; 78.2%; Pred. No. 1e-22;
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 146.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 146.
DN W02004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
QUERTY MATCH

Best Local Similarity 73.2%; Pred. No. 2.2e-21;
RESULT 1324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1329

ID AAL20897 standard; CDNA; 430 BP.

ID Human breast cancer expressed polynucleotide 13354.

PN W0200151628-A2.

PD 19-JUL-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABN65723 standard; cDNA; 531 BP.
Human cancer related polynucleotide SEQ ID NO 5690.
WO200214500-A2.
                                                                                                                                                                                              5.7%; Score 105.8; DB 10; 77.3%; Pred. No. 2.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC27700 standard; cDNA; 438 BP.
Human secreted protein 5' EST, SEQ ID NO: 31775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADR52798 standard, DNA; 136284 BP.
Drug therapy altered expressed gene #149.
WO2004072265-A2.
                                                                                                                                                                                                                                            Human genomic sequence hCG28560. 12-SED-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DORN/) DORNER A J. (TREP/) TREPICCHIO W L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMHP) WYETH.
(BURC/) BURCZYNSKI M.
(TWIN/) TWINE N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
RESULT 1328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local_Similarity
RESULT 1330
                                                                                                                                                                                           Query Match
Best Local Similarity
RESULT 1325
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RESULT 1331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP1033401-A2.
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AAKKS5994 standard; DNA; 59060 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40806.
WO200157182-A2.
                                                                                                                                                                                                          ADJ30876 standard; DNA; 6558 BP.
Human musculoskeletal system-associated genomic DNA - SEQ ID 3503.
US2004009488-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.7%; Score 105.6; DB 12; Length 139389; Best Local Similarity 75.2%; Pred. No. 3.1e-21; RESULT 1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 105.6; DB 11; Length 175077; Pred. No. 3.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.7%; Score 105.6; DB 11; Length 122923; Best Local Similarity 77.9%; Pred. No. 2.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-APR-2002.
(GENE-) GENE LOGIC INC.
ETY MATCH
St Local Similarity 75.2%; Pred. No. 3.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 9; Length 139389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MBK84795 standard; cDNA; 139389 BP.
Human cDNA differentially expressed in granulocytic cells #1366
WO200228999-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0-40G-2001.
(HUMA-) HUMAN GENOME SCI INC.
(ery Match 5.7%; Score 105.6; DB 4; Length 59060;
ery Match 78.2%; Pred. No. 1.8e-21;
                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
ry Match
t Local Similarity 81.7%; Pred. No. 4.8e-22;
                  cDNA encoding novel human musculoskeletal system antigen #2470.
US2002147140-A1.
                                                                                                                                                       5.7%; Score 105.6; DB 8; Length 6558; 81.7%; Pred. No. 4.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADJ31148 standard; cDNA; 139389 BP.
Human malignant pleural mesothelioma (MPM) cDNA #27.
US2003219760-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ISIS-) ISIS PHARM INC.

ry Match S.7%; Score 105.6; DB 6;

t Local Similarity 71.5%; Pred. No. 1.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cuery Match 5.7%; Score 105.6; DB 9. Beet Local Similarity 75.2%; Pred. No. 3.1e-21; RESULT 1348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-MAR-2003.
(BGHM ) BRIGHAM & WOMENS HOSPITAL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-NOV-2003.
(BGHM ) BRIGHAM & WOMENS HOSPITAL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADB70369 standard, cDNA, 139389 BP.
PAC 6802 cDNA SEQ ID NO:61.
WO2003021229-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACN44026 standard; DNA; 122923 BP.
Human genomic sequence hCG24510.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACN44626 standard; DNA; 175077 BP.
Human genomic sequence hCG19724.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABS67634 standard; DNA; 63000 BP.
Human casein kinase-2 genomic DNA.
WO200262818-A2.
  ABX60126 standard; cDNA; 6558 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NYC.2-2-

NYC.2-2-2003.

(SAGR-) SAGRES DISCOVERY.

5.7%;

PIV Match -- 1 arity 78.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
RESULT 1344
                                                                   10-OCT-2002.
(ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 1343
                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-AUG-2002
                                                                                                                                                                                                                                                                                            15-JAN-2004
                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                            AAK66534 standard; DNA; 1448 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21346.
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADI97535 standard, DNA; 5989 BP.
Human respiratory system associated polypeptide-related DNA SeqID999.
US2003077704-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK86101 standard; DNA; 6558 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40913.
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS28565 standard; DNA; 5989 BP.
Genomic seguence #405 encoding for novel human respiratory antigen.
WO200155448-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAL37138 standard; DNA; 6558 BP.
Human musculoskeletal system related polynucleotide SEQ ID NO 3503.
WO200155367-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
ry Match
5.7%; Score 105.6; DB 10; Length 5989;
t Local Similarity 78.2%; Pred. No. 4.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12; Length 3977;
                                                                                                                                                                                                                                                         09-AUG-2001.
A (HUMA-) HUMAN GENOME SCI INC.
Query Match
5.7%; Score 105.6; DB 4; Length 1448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 5989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 5.7%; Score 105.6; DB 5; Length 6558; Best Local Similarity 81.7%; Pred: No. 4.8e-22; RESULT 1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
(FLY Match 5.7%; Score 105.6; DB 4; Length 6558;
ery Match 5.7%; Pred. No. 4.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.7%; Score 105.6; DB 4; Length 5989; 78.2%; Pred. No. 4.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 6558;
                                                                                                                                  Length 658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABAZI372 standard; DNA; 6558 BP.
Human nervous system related polynucleotide SEQ ID NO 13703.
WO200159063-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human respiratory system associated genomic DNA seq id 999. US2003215893-A1. 20-NOV-2003.
                  Human cancer related polynucleotide SEQ ID NO 2511.
WO200214500-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mudan GENOME SCI INC.

Suery Match
Best Local Similarity 81.7%; Score 105.6; DB 4;
RESULT 1340
ID ABA21372 standard; DNa; 6558 BP.
DE Human nervous system related
PD Ho-AUG-200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.7%; Score 105.6; DB 11; Best Local Similarity 78.2%; Pred. No. 4.5e-22; RESULT 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.7%; Score 105.6; DB 1
81.7%; Pred. No. 3.5e-22;
                                                                                                                                5.7%; Score 105.6; DB 6
79.9%; Pred. No. 1.2e-22;
                                                                                                                                                                                                                                                                                                                                                                             AD063489 standard; cDNA; 3977 BP Novel human cDNA sequence #650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REAS-) RES ASSOC BIOTECHNOLOGY.
ABN62544 standard; cDNA; 658 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADG41761 standard; DNA; 5989 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.7%;
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2001.
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LAZ.
2001.
LAZY MATCH
Best Local Similarity 6>
RESULT 1334
ID AD063489 standar'
DE Novel human
PN EP1440°
PD 28-7
                                                                                   (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 1339
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Best Local Similarity
RESULT 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1335
                                                                                                                                                  Best Local Similarity RESULT 1333
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                                                              21-FEB-2002
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Length 63000;

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Best Local Similarity 79.2%; Pred. No. 5.4e-22; RESULT 1359
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Best Local Similarity 79.2%; Pred. No. 3.5e-22;

RESULT 1356

DD ADRO6891 standard; CDNA; 3825 BP.

DE Full length human cDNA useful for treating neurological disease Seq 397.

PN EP147413-A2.
                                                  PD 22-JUL-2004.

PA (SAGR-) SAGRES DISCOVERY INC.

QUERY MATCh

Best Local Similarity 78.2%; Pred. No. 3.6e-21;

RESULT 1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 76.7%; Pred. No. 5.4e-21;
RESULT 1354
                                                                                                                                                                                           OBtecoarthritis-associated polymorphic nucleotide #284.
WO2003054166-A2.
WO2003054166-A2.
013-JUL-2003.
(INCY-) INCYTE GENOMICS INC.
5.7%; Score 105.6; DB 10; Length 190000; at Local Similarity 78.2%; Pred. No. 3.78-21;
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.7%; Score 105.6; DB 13; Length 227246; Best Local Similarity 76.7%; Pred. No. 4.2e-21; RESULT 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA34969 standard; DNA; 6210 BP.
Human adenosine receptor related polynucleotide SEQ ID NO:2658.
WO200009525-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.7%; Score 105.4; DB 13; Length 3825; 79.2%; Pred. No. 4e-22;
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(UYEC-) UNIV EAST CAROLINA.
5.7%; Score 105.4; DB 3; Length 6210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 6210;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAI94396 standard; cDNA; 822 BP.
Human neuroblastoma expressed polynucleotide SEQ ID NO 471.
WO200166719-A1.
       RESULT 1350
ID ADQ97167 standard; DNA; 176771 BP.
DE Human cancer associated sequence HD2-08-009, SEQ ID 143.
PN WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 5.7%; Score 105.4; DB 2; Best Local Similarity 79.2%; Pred. No. 5.4e-22; RESULT 1358
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13-SEP-2001.
(CHS) CHIBA PREFECTURE.
(HISM ) HISAMITSU PHARM CO LTD.
(HISM ) HISAMITSU PHARM CO LTD.
5.7%; Score 105.4; DB 4;
                                                                                                                                                                                                                                                                                                                             ABD33272 standard; DNA; 227246 BP.
Human cancer-associated (CA) gene HD07-047.
WO2004058146-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACN44070 standard; DNA; 344548 BP.
Human genomic sequence hCG36954.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADAS2859 standard; cDNA; 3098 BP.
Human coding sequence, SEQ ID 427.
EP1293569-A2.
                                                                                                                                                                              ADL13752 standard; DNA; 190000 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-AUG-2004.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ63815 standard; cDNA; 6210 BP
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-2004.
(SAGR-) SAGRES DISCOVERY INC.
                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 1355
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EP599077-A2
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Human low adenosine antisense oligonucleotide related sequence #2658. W0200062736-A2. 26-OCT-2000. UVIV BAST CAROLINA. (NYCE.) NIV BAST CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABD20634 standard; DNA; 6210 BP. Human pulmonary and inflammatory target DNA #245. W0200285309-A2. 31-0CT-2002. (BPIG-) EPIGENESIS PHARM INC. 5.7%; Score 105.4; DB 11; Length 6210; st Local Similarity 79.2%; Pred. No. 5.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vuery Match 5.7%; Score 105.4; DB 10; Length 6210; Best Local Similarity 79.2%; Pred. No. 5.4e-22; RESULT 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.7%; Score 105.4; DB 10; Length 6210; 79.2%; Pred. No. 5.4e-22;
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Pred. No. 5.4e-22;
                                                                                                                                                                                                                                                Human breast cancer associated coding sequence SEQ ID NO: 1009 WO200259271-A2.
                                                                                                                                                                                                                                                                                          PD 01-AUG-2002.

PA (GENE.) GENE LOGIC INC.
Query Match
Query Match
Best Local Similarity 79.2%; Pred. No. 5.4e-22;
RESULT 1361

ID ABZ35089 standard; CDNA; 6210 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 201.
PN W0200274979-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 6210;
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Renal cell carcinoma differentially expressed gene #141.
WO2004048933-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 79.2%; Pred. No. 5.4e-22; RESULT 1362
ID ACC46752 standard; CDNA; 6210 BP.
DB HUMAN COPD related protein encoding CDNA SEQ ID NO:3.
PN WO200297127-A2.
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                                                                                                                                                          5.7%; Score 105.4; DB 3; 79.2%; Pred. No. 5.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORTH ) ORTHO CLINICAL DIAGNOSTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 79.2%; Prec
RESULT 1365
ID ADH17136 standard; cDNA; 6210 BP.
                                                                                                                                                                                                                             CDNA; 6210 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABZ96785 standard; DNA; 6210 BP. Human nucleic acid sequence. Woo200285308-A2. 31-OCT-2002. (EPIG-) EPIGENESIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human c-fos proto oncogene cDNA.
WO2003097854-A2.
LT 1359
AAF21091 standard; DNA; 6210 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TWIN/) TWINE N C.
(BURC/) BURCZYNSKI M E
(TREP/) TREPICCHIO W L.
(DORN) DORNER A.
(STOV/) STOVER J A.
(SLON/) SLONI D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 1367
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RESULT 1363
                                                                                                                                                                            Best Local Similarity
RESULT 1360
ID ABT10875 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-NOV-2003.
(SUGE-) SUGEN INC.
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Query Match
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23-OCT-2003
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                                                                                                                                                                                                                                        12-SEP-200
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Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:84.
WO200116311-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF97871 standard; DNA; 23241 BP.
Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:85.
                                                                                                                                                                                                                                                                                                                                                                        AAF21095 standard; DNA; 16595 BP.
Human low adenosine antisense oligonucleotide related sequence #2662.
W020062736-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 16595;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.7%; Score 105.4; DB 11; Length 22477; 79.2%; Pred. No. 1.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.7%; Score 105.4; DB 3; Length 16595; 79.2%; Pred. No. 9.8e-22;
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Pred. No. 1.2e-21;
                                                                                                                                                                           Length 6210;
                                                                                                                                                                                                                               AAA34973 standard; DNA; 16595 BP.
Human adenosine receptor related polynucleotide SEQ ID NO:2662
WO200009525-A2.
                                                                                                                                                                                                                                                                                                                                     Score 105.4; DB 3; Length 16595; Pred. No. 9.8e-22;
                                                                                                                                                                        Score 105.4; DB 13;
Pred. No. 5.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 105.4; DB 12;
Pred. No. 1.7e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 105.4; DB 5;
Pred. No. 1.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABD20638 standard; DNA; 16595 BP.
Human pulmonary and inflammatory target DNA #249.
WO200285309-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-2002.
(EPIG-) EPIGENESIS PHARM INC.
(EPIG-) EPIGENESIS PHARM INC.
(EPY Match 5.7%; Score 105.4; DB 11
(EPIG-) Similarity 79.2%; Pred. No. 9.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-2002.
(EPIG-) EPIGENESIS PHARM INC.
(EPIG-) EPIGENESIS PHARM INC.
5.7%; Score 105.4; DB 10ery Match
5.7%; Pred. No. 9.8e-22;
ADR52837 standard; DNA; 6210 BP.
Drug therapy altered expressed gene #188.
WO2004072265-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA; 16595 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACN44910 standard; DNA; 22477 BP
Human genomic sequence hCG22355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HISM ) HISAMITSU PHARM CO LTD. (CHIB-) CHIBA PREFECTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HISM ) HISAMITSU PHARM CO LTD. (CHIB-) CHIBA PREFECTURE.
                                                                                                                                                                           5.7%;
                                                                                                                                                                                                                                                                                                                                   5.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human nucleic acid sequence.
                                                                                                                                                                                                                                                                                           24-FEB-2000.
(UYEC-) UNIV EAST CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYEC-) UNIV EAST CAROLINA. (NYCE/) NYCE J W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SAGR-) SAGRES DISCOVERY
                                                                                                                                    (DORN/) DORNER A J.
(TREP/) TREPICCHIO W L.
                                                                           (AMHP ) WYETH.
BURC/) BURCZYNSKI M.
(TWIN/) TWINE N.
                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
RESULT 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
RESULT 1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABZ96789 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003073826-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200285308-A2.
                                                                                                                                                                           Match
                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                 RESULT 1368
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12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
S-TY Match 5.7%; Score 105.4; DB 11; Length 122923;
The treat Similarity 79.2%; Pred. No. 3.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INCY-) INCYTE GENOMICS INC.
ry Match
t Local Similarity 77.6%; Pred. No. 3.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 110000;
                                                                                                                                                                                                                                                                                         (SAGR-) SAGRES DISCOVERY.

ry Match 5.7%; Score 105.4; DB 11; Length 73967;

t Local Similarity 79.2%; Pred. No. 2.4e-21;
                                                                                               (INCY-) INCYTE GENOMICS INC.

5.7%; Score 105.4; DB 10; Length 41369; t Local Similarity 74.2%; Pred. No. 1.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 94752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH92222 standard; DNA; 700 BP.
Human inflammatory bowel disease related gene fragment IGR2234a.
WQ200142511-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS42054 standard; DNA; 10085 BP.
Genomic sequence #370 encoding novel human enzyme polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 105.2; DB 4; Length 574; Pred. No. 1.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 629;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADL13941 standard; DNA; 125515 BP. Osteoarthritis-associated polymorphic nucleotide #473.
ADL13522 standard; DNA; 41369 BP.
Osteoarthritis-associated polymorphic nucleotide #54.
03-030354166-A2.
03-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABN63732 standard; cDNA; 629 BP.
Human cancer related polynucleotide SEQ ID NO 3699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.7%; Score 105.4; DB 12; 79.2%; Pred. No. 3.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CELL-) CELLTECH R & D INC.
(UYRO-) UNIV ROTTERDAM BRASMUS.
PY Match 5.7%; Score 105.4; DB 10;
t Local Similarity 73.4%; Pred. No. 2.8e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 105.2; DB 6;
Pred. No. 1.5e-22;
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                                                                                                                                                                                                                                                                                                                                                                                            ADF11646 standard; DNA; 94752 BP.
Human chromosome 17 clone HPRC905N1 nucleic acid
WO2003087763-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cDNA clone (3'-primer) SEQ ID NO:7397.
EP10.4617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (WHED ) WHITEHEAD INST BIOMEDICAL RES. (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACN44026 standard; DNA; 122923 BP.
Human genomic sequence hCG24510.
WO2003073826-A2.
                                                                                                                                                                                               ACN44438 standard; DNA; 73967 BP. Human genomic sequence hCG27607. WO2003073826-A2.
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(HELI-) HELIX RES INST.
5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.7%;
76.9%;
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                                                                                                                                            Best Local Similarity RESULT 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 1380
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Human genomic DNA encoding partial novel secreted protein, Seq ID 1698.
WO200155322-A2.
                                         02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
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(ROSE/) ROSEN C A.
(RUBI/) RUBIN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                               (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
RESULT 1399
                                                                                                                                                                                                                                                                                        Local Similarity
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RESULT 1402
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Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27984
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAK70102 standard; DNA; 16555 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24914
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAK71070 standard; DNA; 17874 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25882.
WO200157182-A2.
                                                                                                                                                                                                                                                                      AAL37624 standard; DNA; 12452 BP.
Human musculoskeletal system related polynucleotide SEQ ID NO 3989.
WO200155367-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADJ31362 standard; DNA; 12452 BP.
Human musculoskeletal system-associated genomic DNA - SEQ ID 3989
US2004009488-A1.
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(HUMA-) HUMAN GENOME SCI INC.
ery Match 5.7%; Score 105.2; DB 4; Length 17874;
                                                                                                                                                                     02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ery Match
5.7%; Score 105.2; DB 4; Length 10085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-40G-2001.
(HUMA-) HUMAN GENOME SCI INC.
ery Match
5.7%; Score 105.2; DB 4; Length 16555;
ery Match
5.7%; Score 105.2; Length 16555;
                                                             Length 10085;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 12452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABX60612 standard; cDNA; 12452 BP.
cDNA encoding novel human musculoskeletal system antigen #2956.
US2002147140-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.7%; Score 105.2; DB 8; Length 12452; 78.5%; Pred. No. 9.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 16555;
                       Best Local Similarity 80.2%; Score 105.2; DB 4; Length 1008 RESULT 1386 ED STANDALOS BP. BESULT 1386 ED STANDALOS BP. BE Human reproductive system related antigen DNA SEQ ID NO: 5491. PD 02-AUG-2001. PA (HUMA-) HIMAN TO STANDALOS BP. BP. CAUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                          ABA21062 standard; DNA; 12452 BP.
Human nervous system related polynucleotide SEQ ID NO 13393.
WO200159063-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
5.7%; Score 105.2; DB 5;
lery Match
5.7%; Pred. No. 9.5e-22;
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ry Match
5.7%; Score 105.2; DB 4;
t Local Similarity 82.1%; Pred. No. 1.1e-21;
                 02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
6ry Match 5.7%; Score 105.2; DB 4;
ery Match 80.2%; Pred. No. 8.4e-22;
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(HUMA-) HUMAN GENOME SCI INC.

6-ry Match 5.7%; Score 105.2; DB 1.

5.7%; Pred. No. 9.58-22;
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                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
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RESULT 1392
                                                                                                                                                                                                                              Best Local Similarity RESULT 1387
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Best Local Similarity
RESULT 1389
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RESULT 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
RESULT 1393
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Best Local Similarity
RESULT 1390
       WO200155301-A2.
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AASS6966 standard; DNA; 25619 BP.
Human genomic DNA encoding partial novel secreted protein, Seq ID 302.
WO200155441-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAK70103 standard; DNA; 23885 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24915.
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                        RESULT 1396

LD AAK73173 standard; DNA; 23885 BP.

DB Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27985.

PN WO200157182-A2.
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(CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
5.7%; Score 105.2; DB 3; Length 25871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-AuG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ery Match 5.7%; Score 105.2; DB 4; Length 25619;
st Local Similarity 78.5%; Pred. No. 1.5e-21;
Match 5.7%; Score 105.2; DB 4; Length 19472; Local Similarity 74.1%; Pred. No. 1.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 25619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6; Length 25619;
                                                                                                                                                                                                                                                                    Length 19472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 23885;
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Human reproductive system related antigen DNA SEQ ID NO:
W0200155320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 5.7%; Score 105.2; DB 4;

Best Local Similarity 82.1%; Pred. No. 1.4e-21;

RESULT 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
5.7%; Score 105.2; DB 5;
it Local Similarity 78.5%; Pred. No. 1.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                            PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

QUENTY MATCh

5.7%; Score 105.2; DB 4;

Best Local Similarity 82.1%; Pred. No. 1.4e-21;

RESULT 1397
                                                                                                                                                                                                                                                                    5.7%; Score 105.2; DB 8; 74.1%; Pred. No. 1.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
ry Match
t Local Similarity 78.5%; Pred. No. 1.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.7%; Score 105.2; DB 6, 78.5%; Pred. No. 1.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK72116 standard; DNA; 25619 BP.
Human ovarian antigen #15 genomic sequence #1.
WO200155329-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK91708 standard; DNA; 25619 BP.
Novel ovarian related polynucleotide #17.
US2002045230-A1.
                                                                             ABX74073 standard; DNA; 19472 BP. Human novel polynucleotide #901. US2002132753-A1.
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Human genomic OCTN2 sequence.
WO200014210-A1.
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YOUNG P E.
FERRIE A M.
                                                                                                                                                                                                          Best Local Similarity
RESULT 1413
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RESULT 1418
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RESULT 1419
                                                                              GREENE J M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADS89043 standard;
                                                                                                                                             (FLOR/) FLORENCE
(EBNE/) EBNER R.
(OLSE/) OLSEN H.
                                                                                                                                                                                                                                                                                               09-AUG-200
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                                                                                                                           (YUGG/)
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DNA fragment of a BAC clone that encodes a human secreted protein Seq726.
US2004010132-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADF13118 standard; DNA; 161652 BP.
Hypermethylation site in human breast cancer CpG island locus HBC-48.
US2003129602-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1411
ID AAK72510 standard; DNA; 429 BP.
DE Human immune/haematopoletic antigen genomic sequence SEQ ID NO:27322
PN WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.7%; Score 105.2; DB 12; Length 161652; 78.5%; Pred. No. 4.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 161652;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 110000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 105.2; DB 10; Length 110000;
Pred. No. 3.6e-21;
                                                                                                                                                                                                                                                                                     03-040.2003.
03-040.2003.
(INCY-) INCYTE GENOMICS INC.
ery Match
5.7%; Score 105.2; DB 10; Length 47188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 54701;
                                                                                                                                                                                            DB 9; Length 26850;
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                                                                                                                                                                                                                                           ADL13758 standard; DNA; 47188 BP.
Osteoarthritis-associated polymorphic nucleotide #290.
WO2003054166-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.7%; Score 105.2; DB 12; 78.5%; Pred. No. 4.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 105.2; DB 10;
Pred. No. 3.6e-21;
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                                                                                                                                                                                              5.7%; Score 105.2; DB 9 76.9%; Pred. No. 1.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 105.2; DB 1:
Pred. No. 2.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 5.7%; Score 105.2; DB 1:
Best Local Similarity 82.1%; Pred. No. 5.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WOACCEDOIL

09-AUG-2001.

(HUMAL) HUMAN GENOME SCI INC.

5.7%; Score 105; DB 4;

6ry Match

5.7%; Pred. No. 1.4e-22;
                                                                          76.9%; Pred. No. 1.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AD137264 standard; DNA; 161652 BP.
Hypermethylation in cancer (HBC) locus-48.
US6605432-B1.
                                                                                                                                                                            (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP
                                                                                                        ACF05020 standard; DNA; 26850 BP.
Human cation transporter OCTN2 gene.
WWO2003054011-A2.
03-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACN44754 standard; DNA; 215221 BP.
Human genomic sequence hCG37990,
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                            ACN4478 standard; DNA; 54701 BP.
Human genomic sequence hCG24071.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.78;
74.18;
                                                                                                                                                                                                                                                                                                                                                                                                                    WOADLOWS
12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
GARY MATCH ---1arity 76.9%;
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Best Local Similarity
RESULT 1403
ID ACF05020 standa
DE Human catir
PN WO2003r
PD 03
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(RUBE/) RUBEN S M.
(FLOR/) FLORENCE K A.
                                                                                                                                                                                                        Best Local Similarity RESULT 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 1410
                                                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 1405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROSEN C A.
BREWER L A.
DUAN R D.
RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
RESULT 1407
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Best Local Similarity
RESULT 1408
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                                                                                                                                                                                              Query Match
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(BREW/)
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Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27117.
WO200157182-A2.
                                                                                                                                                                             Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37597.
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAK87529 standard; DNA; 13608 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42341
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL98096 standard; DNA; 4026 BP.
Human testicular antigen encoding DNA fragment SEQ ID NO: 2748.
WO200155317-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 10224;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAL05213 standard; DNA; 4026 BP.
Human reproductive system related antigen DNA SEQ ID NO: 7901
WO200155320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUWA-) HUMAN GENOME SCI INC.
ry Match 5.7%; Score 105; DB 4; Length 13608;
t Local Similarity 77.8%; Pred. No. 1.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.7%; Score 105; DB 4; Length 4026;
Best Local Similarity 73.4%; Pred. No. 5.5e-22;
RESULT 1417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 4026;
                                                                                           Length 429;
                                                                                                                                                                                                                                                                                Length 1276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3252;
                                                                                           5.7%; Score 105; DB 12; 79.5%; Pred. No. 1.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.7%; Score 105; DB 10; 76.3%; Pred. No. 9.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 105; DB 13;
Pred. No. 9.8e-22;
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Pred. No. 1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.

ry Match 5.7%; Score 105; DB 4;

t Local Similarity 77.8%; Pred. No. 4.9e-22;
                                                                                                                                                                                                                                                                           5.7%; Score 105; DB 4; 76.7%; Pred. No. 2.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
ry Match 5.7%; Score 105; DB 4;
t Local Similarity 73.4%; Pred. No. 5.5e-22;
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                                                                                                                                                              AAK82785 standard; DNA; 1276 BP
                                                                                                                                                                                                                                                                                                                                                 AAK72305 standard; DNA; 3252 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human RASSF1 gene SEQ ID NO:59.
WO2004035803-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WOZOUZE
29-APR-2004.
(EPIG-) EPIGENOMICS AG.
5.7%;
                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
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PA (EPIG-) EPIGENOMICS AG.

QUEYY MATCh 5:7%;

Best Local Similarity 76.3%;

RESULT 1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RASSF1 genomic DNA region.
WO2003072821-A2.
04-SEP-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADS89114 standard; DNA; 1
Human gene SEQ ID NO:130.
WO2004035803-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EPIG-) EPIGENOMICS AG.
YU G.
FLORENCE C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 1415
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RESULT 1430
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Human thyroid tumour associated PKCG genomic sequence SEQ ID NO: 18.
WO200283727-A2.
                                                                                                                                                  D1872656 standard; DNA; 23328 BP.

Human FUS1 gene.

W2203008583-A2.
30.JAN-2003.

(SAGR-) SAGRES DISCOVERY.

FT Match

St. Local Similarity 76.3%; Pred. No. 1.6e-21;
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Pred. No. 1.8e-21;
                                                                                                                                                                                                                                                                                                                                                                              Length 23328;
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                                                                                                       Length 23328;
RESULT 1421

ID ADA02918 standard; DNA; 23328 BP.

DE Human FUS1 carcinoma associated gene, SEQ ID NO.1436.

PN WO2003657146-A2.

PD 17-JUL-2003.

PA (SAGRES DISCOVERY.

Query Match

Best Local Similarity 76.3%; Pred. No. 1.6e-21;

RESULT 1422.

ID ADB72656 standard; DNA; 23328 BP.

PN WO200308583-A2.

PN WO200308583-A2.

PN (SAGRE) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA02924 standard, DNA, 27589 BP.
Human RASSF1 carcinoma associated gene, SEQ ID NO:1442
WO2003057146-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AD001541 standard; DNA; 25301 BP.
Human protein kinase C gamma (PRKCG) genomic DNA.
US2004106138-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human carcinoma associated (CA) nucleic acid #91 US2004072154-A1.
                                                                                                                                                                                                                                                                                                                                     05-JUN-2003.
(SAGR-) SAGRES DISCOVERY.
ery Match 5.7%; Score 105; DB 10;
ery Match 76.3%; Pred. No. 1.6e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 105; DB 12;
Pred. No. 1.7e-21;
                                                                                                                                                                                                                                                                                         DNA; 23328 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                               ADM74513 standard; DNA; 23328 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC85404 standard; DNA; 27589 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB72662 standard; DNA; 27589 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Rassfl genomic sequence WO2003045230-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.7%;
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WO2003045230-A2.
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(SAGR-) SAGRES DISCOVERY.
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(SAGR-) SAGRES DISCOVERY.
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(UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-APR-2004.
(MORR/) MORRIS D W.
(ENGE/) ENGELHARD E K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRAPATORY

ACR/) MORRIS D W.

(ENGE/) ENGELHARD E

Query Match

BEST Local Similarity

RESULT 1425

ID ABZ20990 stand**

DE Human thyre*

PN WO2002**

PD 24-*

PA
                                                                                                                                                                              Best Local Similarity
RESULT 1426
ID AD001541 standard; DN:
DE Human protein Kinase (
PN US2004106138-A1.
PD 03-UUN-2004.
PA (UNIW ) UNIV WASHINGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-OCT-2002.
(BULL/) BULLERDIEK J.
Query Match
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
RESULT 1424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1429
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Best Local Similarity
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Best Local Similarity
RESULT 1427
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WO2003008583-A2.
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Genomic sequence #428 encoding novel human connective tissue polypeptide. WO200155343-A1.
                                                                                                                              5.7%; Score 105; DB 12; Length 27589; 76.3%; Pred. No. 1.8e-21;
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Human reproductive system related antigen DNA SEQ ID NO: 8319.
WO200155320-A2.
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5.7%; Score 105; DB 4; Length 32192;

it Local Similarity 73.6%; Pred. No. 2e-21;
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(HUMA) HUMAN GENOME SCI INC.
127 Match 5.7%; Score 105; DB 4; Length 32192;
st Local Similarity 73.6%; Pred. No. 2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ery Match 5.7%; Score 105; DB 4; Length 32192;
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Human nervous system related polynucleotide SEQ ID NO 7659.
WO200159063-A2.
                                                                                                                                                                                                                                                                                                                                                                AALO5532 standard; DNA; 32192 BP.
Human reproductive system related antigen DNA SEQ ID NO:
WO200155320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AALOS257 standard, DNA, 32192 BP.
Human reproductive system related antigen DNA SEQ ID NO:
WO200155320-A2.
ADM74519 standard; DNA; 27589 BP.

Human carcinoma associated (CA) nucleic acid #94
US2004072154-A1.
15-APR-2004.

(MORX) MORXIS D W.

(ENGE/) ENGELHARD E K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 105; DB 11;
Pred. No. 3.2e-21;
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20-MAR-2003.
(HUMA-) HUMAN GENOME SCI INC.
5.7%; Score 105; DB 9;
ery Match
5.7%; Score 105; DB 9;
                                                                                                                                                                                                                                                 02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
5.7%; Score 105; DB 4;
ery Match 5.7%; Pred. No. 2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.7%; Score 105; DB 5; Best Local Similarity 73.6%; Pred. No. 2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.

ry Match

5.7%; Score 105; DB 4;

t Local Similarity 73.6%; Pred. No. 2e-21;
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ID ADBG068S standard, DNA; 32192 BP.
DB Connective tissue related genomic DNA #428.
PN US2003054375-Al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL98141 standard; DNA; 32192 BP.
                                                                                                                                                                                            DNA; 32192 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity, 77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
RESULT 1435
                                                                                                                                             Best Local Similarity RESULT 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
RESULT 1434
                                                                                                                                                                                                                                                                                                               Best Local Similarity
RESULT 1432
                                                                                                                                                                                          ABK42529 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-AUG-2001
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Best Local Si
RESULT 1433
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                                                                                                                            Query Match
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ABD32843 standard; DNA; 326002 BP.
Human cancer-associated genomic DNA HD17-014.
WC2004074320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA; 11336 BP.
                                                                                                                                                                                                                                                                                                          ADQ25315 standard; DNA; 2988 BP.
                                                                                                                                                                                                                                                                                                                                                                                  (PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match
Local Similarity 77.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human protein DNA #192.
US2002168711-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAY-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TULA-) TULARIK INC.
                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADB94583 standard;
                                                                                                                                                                                                                                                                                                                                            WO2004048938-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JUL-2004.
(SAGR-) SAGRES DISCOVERY INC.
ery Match 5.7%; Score 105; DB 12; Length 128963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 95914;
                                                                                                       Score 105; DB 11; Length 70242; Pred. No. 3.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.7%; Score 105; DB 10; Length 96589;
Best Local Similarity 73.8%; Pred. No. 3.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 96589;
                                                                                                                                                                                                                                                                                                                                                                                                   Length 84539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 96589;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 96589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA02954 standard; DNA; 96589 BP.
Human NR3C1 carcinoma associated gene, SEQ ID NO:1472.
WO2003057146-A2.
                                                                                                                                                                                                                                                                                                        ADL13479 standard; DNA; 84539 BP.
Osteoarthritis-associated polymorphic nucleotide #11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86
                                                                                                                                                          ABL64158 standard; DNA; 84539 BP.
Stomach cancer related gene sequence SEQ ID NO:2495.
MWO20194629-A2.
13-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human carcinoma associated (CA) nucleic acid #109.
US2004072154-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADQ97110 standard; DNA; 128963 BP.
Human cancer associated sequence HD08-002, SEQ ID
WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.7%; Score 105; DB 13; 77.8%; Pred. No. 3.8e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 105; DB 10;
Pred. No. 3.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 105; DB 12;
Pred. No. 3.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                   5.7%; Score 105; DB 10; 77.8%; Pred. No. 3.6e-21;
                                                                                                                                                                                                                                                    5.7%; Score 105; DB 6; 77.8%; Pred. No. 3.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 105; DB 9;
Pred. No. 3:9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABD33444 standard; DNA; 95914 BP.
Human cancer-associated (CA) gene HD07-084.
WO2004058146-A2.
               ACN44710 standard; DNA; 70242 BP.
Human genomic sequence hCG1784894
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADB72692 standard; DNA; 96589 BP.
Human NR3C1 gene.
WO2003008583-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA; 96589 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC85434 standard; DNA; 96589 BP
                                                              NCS-SEP-2003.
(SAGR.) SAGRES DISCOVERY.
(SAGR.) SAGRES TS-28;
(ery Match 72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SAGR-) SAGRES DISCOVERY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 73.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAGRES DISCOVERY.
5.7%;
Similarity 73.8%;
                                                                                                                                                                                                                                                                                                                                                                                (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Nr3cl genomic sequence WO2003045230-A2.
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(SAGR-) SAGRES DISCOVERY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MORR/) MORRIS D W. (ENGE/) ENGELHARD E K.
                                                                                                                                                                                                                                   (AVAL-) AVALON PHARM.
                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 1441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                         Query Match
Best Local Similarity
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                            WO2003054166-A2.
03-JUL-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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RESULT 1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1443
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RESULT

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AAS27780 standard; DNA; 11336 BP.
DNA encoding novel signal transduction pathway protein, Seg ID 1440.
WO200154733-A1.
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Human sequence from clone RP5-1009E24 on chromosome 20 Contains DNA.
WO2003072827-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-SEP-2003.
(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 5.7%; Score 104.8; DB 11; Length 57038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.7%; Score 104.8; DB 10; Length 11336; 82.4%; Pred. No. 1.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.7%; Score 104.8; DB 12; Length 7136; 77.2%; Pred. No. 9.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-40G-2001.
(HUMA-) HUMAN GENOME SCI INC.
ery Match 5.7%; Score 104.8; DB 4; Length 11336;
ery Match 82.4%; Pred. No. 1.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13; Length 7136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 7136;
                                                      Length 326002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.7%; Score 104.8; DB 12; Length 2988; 77.2%; Pred. No. 5.4e-22;
                                                                                                                                                                                                                                                                                DB 4; Length 552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADF83102 standard; cDNA; 7136 BP.
Human Pellino homologue 1 gene, overexpressed in cancer.
WO2003100000-A2.
                                                                                                                                                                                                                                                                                                                                                                                       Human soft tissue sarcoma-upregulated DNA - SEQ ID 8135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 5.7%; Score 104.8; DB 13; Local Similarity' 77.2%; Pred. No. 9.1e-22;
PD 02-SEP-2004.

PA (SAGR-) SAGRES DISCOVERY INC.

QUERY MAtch

5.7%; Score 105; DB 13;

Best Local Similarity 81.3%; Pred. No. 8.1e-21;

RESULT 1449
                                                                                                                                                                                                                 07-FEB-2001.
(HELL-) HELIX RES INST.
5.7%; Score 104.8; DB 4.ery Match
et Local Similarity 78.8%; Pred. No. 1.9e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 104.8; DB 1:
Pred. No. 9.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADP24928 standard; cDNA; 7136 BP.
PRO polypeptide encoding cDNA SEQ ID NO:2106.
WO2004041170-A2.
                                                                                                                        AAH09669 standard; cDNA; 552 BP.
Human cDNA clone (3'-primer) SEQ ID NO:6504.
EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADP56419 standard; cDNA; 7136 BP.
Human PRO cDNA sequence SEQ ID NO:2395.
WO2004039956-A2.
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Human macroprotein 10.01-encoding cDNA

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AAKBYOB6 standard; DNA; 1235 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41898.
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUL-2004.
(SAGR-) SAGRES DISCOVERY INC.
ery Match
5.7%; Score 104.8; DB 12; Length 138627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11; Length 181684;
                                                                                                                                                                                                                                                               Length 106378;
                                                                                                                                                                                                                                                                                                                   DB 13; Length 110000;
                                                                                                                                                                                                                                                                                                                                                                     DB 13; Length 110000;
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                                                                                                                           DB 11; Length 92794;
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29-WXY-2003.
(MILL-) MILLENNIUM PHARM INC.
ery Match 5.7%; Score 104.6; DB 11; Length 884;
ery Match 72.2%; Pred. No. 3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PD 09-AGC 2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
BEST Local Similarity 78.1%; Pred. No. 3.6e-22;
ID ABO77944 ctra----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.7%; Score 104.6; DB 4; Length 387;
                                 ADP65471 standard; DNA; 92794 BP.
Human sequence from clone RP5-1009E24 on chromosome 20 DNA.
WO20120227-21.
04-SEP-2003.
(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cancer associated sequence HD08-011, SEQ ID 159. WO2004060304-A2.
                                                                                                                                                                                                                                                                 DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAL12012 standard; cDNA; 387 BP.
Human breast cancer expressed polynucleotide 4469.
WO200151628-A2.
19-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 78.8%; Pred. No. 6.6e-21;
EESULT 146
ID ADP75188 standard; DNA; 276820 BP.
DE Human ADAMTS2 gene.
PN WO2003031594-A2.
PD 17-APR-2003.
                                                                                                                           5.7%; Score 104.8; DB 11
80.5%; Pred. No. 4.4e-21;
                                                                                                                                                                                                                                                               Score 104.8; DB 11
Pred. No. 4.8e-21;
                                                                                                                                                                                                                                                                                                                                                                   Score 104.8; DB 13
Pred. No. 4.9e-21;
                                                                                                                                                                                                                                                                                                                 Score 104.8; DB 1:
Pred. No. 4.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.7%; Score 104.8; DB 1.77.2%; Pred. No. 8.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.7%; Score 104.6; DB 4 72.2%; Pred. No. 1.8e-22;
     80.5%; Pred. No. 3.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Breast cancer related marker, seq id 3350.
US2003099974-Al.
                                                                                                                                                                        ACN44930 standard; DNA; 106378 BP.
Human genomic sequence hCG1742422.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACN44374 standard; DNA; 181684 BP.
Human genomic sequence hCG16651.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                    ADQ97183 standard; DNA; 138627 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACN82200 standard; DNA; 884 BP.
                                                                                                                                                                                                                 5.7%;
                                                                                                                                                                                                                                                                                                                                                                 5.7%;
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(SAGR-) SAGRES DISCOVERY.
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Best Local Similarity
RESULT 1466
ID AAK87086 standard; DN;
DE Human immune/haematope
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 1462
Best Local Similarity
RESULT 1457
                                                                                                                       Query Match
Best Local Similarity
RESULT 1458
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                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity
RESULT 1459
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Best Local Similarity
RESULT 1460
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Best Local Similarity
RESULT 1461
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ABA07013 standard; DNA; 32134 BP.
Human ovarian and breast cancer associated polynucleotide SEQ ID NO 608.
WO200155325-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJIGASS standard; DNA; 16509 BP.
Human isoprenylcysteine carboxyl methyltransferase genomic DNA SeqID 11.
US2003228688-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAKTIG62 standard, DNA, 19243 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26474
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-DEC-2003.
(ISIS-) ISIS PHARM INC.
E-ry Match
5.7%; Score 104.6; DB 12; Length 16509;
ist Local Similarity 78.1%; Pred. No. 1.8e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PD 30-MAY-2003

PA (EPIG-) EPIGENOMICS AG.

Query Match 5.7%; Score 104.6; DB 10; Length 7558;

Best Local Similarity 78.1%; Pred. No. 1.1e-21;

RESULT 1471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.

5.7%; Score 104.6; DB 4; Length 32134;

it Local Similarity 78.1%; Pred. No. 2.7e-21;
                                                                                                                                                                                                                                                                       Length 2820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 32134;
                                                                                                                                                                                                                                                                                                            ID AAH18641 standard; CDNA; 3049 BP.

DE Human CDNA sequence SEQ ID NO:18867.

PD 07-FEB-2001.

PA (HELI-) HELIX RES INST.

Query Match

Best Local Similarity 78.1%; Score 104.6; DB 4; Length 3049;

RESULT 1470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 19243;
                                         PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
QUECY MARCH
5.7%; Score 104.6; DB 6; Length 1568;
Best Local Similarity 62.3%; Pred. No. 4.2e-22;
RESULT 1468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AALOS543 standard; DNA; 8040 BP.
Human reproductive system related antigen DNA SEQ ID NO: 8231.
WO200155320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAL03615 standard; DNA; 32134 BP.
Human reproductive system related antigen DNA SEQ ID NO: 6303.
WO200155320-A2.
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Human reproductive system related antigen DNA SEQ ID NO: 6304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 8040
                                                                                                                                                                                                                      PD 18-SEP-2002.

PA (SHAN-) SHANGHAI INST ONCOLOGY.

Query Match 5.7%; Score 104.6; DB 10;

Best Local Similarity 78.1%; Pred. No. 6e-22;

RESULT 1469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G2-AGG-2001.
(HUWA-) HUMAN GENOME SCI INC.
5.7%; Score 104.6; DB 4;
GTY Match imilarity 69.3%; Pred. No. 1.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
PTY MATCH 5.7%; Score 104.6; DB 4;
st Local Similarity 75.1%; Pred. No. 1.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
ry Match
t Local Similarity 78.1%; Pred. No. 2.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE84040 standard; DNA; 7558 BP.
5' regulatory region of human gene BAK1.
WO2003044226-A2.
                                                                                                                                  ADF48653 standard; cDNA; 2820 BP.
Human PP7518 cDNA #SEQ ID 10.
CN1369505-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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CN1345817-A
24-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-AUG-2001
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Query Match 5.7%;
Best Local Similarity 78.1%;
                  SAGRES DISCOVERY.
                                                                                                                                                         21-MAY-2004.
(SACK/) SACKTOR T C.
(CRAR/) CRARY J F.
(HERN/) HERNANDEZ A I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 1494
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                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 1487
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                                                                                                                                                                                                                                                                                                                                                                            WO2003054166-A2.
03-JUL-2003.
                                                                                                                                                                                                                                       (MIRR/) MIRRA S.
                                                                                                                                                                                                                                                         (SHAO/) SHAO C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200268690-A1.
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                                                                                                                ABA07814 standard; DNA; 32191 BP.
Human ovarian and breast cancer associated polynucleotide SEQ ID NO 609.
WO200155325-A2.
                                                                                                                                                                                                                                                                        AAKK4974 standard; DNA; 35871 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39786.
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                   AAK74751 standard; DNA; 36485 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29563.
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23770 WO200157182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADJ10262 standard; DNA; 51001 BP.
Human geranylgeranyl diphosphate synthase 1 genomic DNA SeqID 11.
US2004005570-A1.
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(ISIS-) ISIS PHARM INC.

1. Autch

1. Autch

1. Local Similarity 78.1%; Pred. No. 3.5e-21;
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                                                           DB 4; Length 32191;
                                                                                                                                                                                                                   Length 32191;
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Human cancer associated sequence HD10-013, SEQ ID 582.
WO2004060304-A2.
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Pred. No. 3.7e-21;
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ry Match

t. Local Similarity 76.6%; Pred. No. 2.9e-21;
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(HUMA-) HUMAN GENOME SCI INC.
Ery Match 5.7%; Score 104.6; DB 4;
ery Match 76.6%; Pred. No. 2.9e-21;
                                                                                                                                                                                                                                                                                                                             09-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ETY MATCH 5.7%; Score 104.6; DB 4
ETY MATCH 78.1%; Pred. No. 2.8e-21;
                                                         5.7%; Score 104.6; DB 4 78.1%; Pred. No. 2.7e-21;
                                                                                                                                                                                          (HUMAN JENOME SCI INC.

5.7%; Score 104.6; DB 4

t Local Similarity 78.1%; Pred. No. 2.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACN43926 standard; DNA; 53242 BP.
Human genomic sequence hCG1782215.
WO2003073826-A2.
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Human genomic sequence hCG1640505
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACN44918 standard; DNA; 55114 BP.
Human genomic sequence hCG20493.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAK68958 standard; DNA; 36485 BP
                                    (HUMA-) HUMAN GENOME SCI INC.
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(SAGR-) SAGRES DISCOVERY INC.
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h
Similarity 78.1%;
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                                                                     Best Local Similarity RESULT 1477
                                                                                                                                                                                                                   Query Match
Best Local Similarity
RESULT 1478
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Best Local Similarity
RESULT 1479
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Best Local Similarity
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WO200155320-A2.
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Human genomic sequence hCG33130.

WO2003073826-A2.
12-SEP-2003.

SAGRE) SAGRES DISCOVERY.

S.7%: Score 104.6; DB 11; Length 110000; t Local Similarity 79.8%; Pred. No. 5.6e-21;
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(SAGR-) SAGRES DISCOVERY.
ETY Match 5.7%; Score 104.6; DB 11; Length 129042;
st Local Similarity 72.7%; Pred. No. 6.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.7%; Score 104.6; DB 13; Length 161051; 76.6%; Pred. No. 7.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 104.6; DB 11; Length 75839;
Pred. No. 4.5e-21;
                                                                                                                                                                                                                                                                      5.7%; Score 104.6; DB 12; Length 80928; 73.8%; Pred. No. 4.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                           (INCY-) INCYTE GENOMICS INC.

ry Match 5.7%; Score 104.6; DB 10; Length 95240;

t Local Similarity 78.1%; Pred. No. 5.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ISIS-) ISIS PHARM INC.

ry Match 5.7%; Score 104.6; DB 7; Length 98844;

t Local Similarity 78.1%; Pred. No. 5.3e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUŬ59434 standard; DNA; 169659 BP.
Human cancer-associated (CA) gene sequence SEQ ID NO:70.
WO20006888-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ84099 standard; DNA; 98844 BP.
Human WRN (RECQL3) helicase genomic DNA - exons 1-20.
                                                                                                                                                                                                                                                                                                                                                             Osteoarthritis-associated polymorphic nucleotide #88
                                                                                   Human protein kinase C iota/lambda genomic sequence WO2004041212-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABD32811 standard; DNA; 161051 BP.
Human cancer-associated genomic DNA HD16-063.
WO2004074320-A2.
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EP1074617-A2.
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                                         RESULT 1486
ID AD025290 standard; DNA; 80928 BP
                                                                                                                                                                                                                                                                                                                                        ADL13556 standard; DNA; 95240 BP.
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07-FEB-2001.
(HELL-) HELIX RES INST.
5.7%;
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(SAGR-) SAGRES DISCOVERY INC.
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ABK42351 standard; DNA; 10248 BP.
Genomic sequence #250 encoding novel human connective tissue polypeptide.
WO200155343-A1.
AAK81852 standard; DNA; 3683 BP.
Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36664.
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                              Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36665.
WO200157182-A2.
                                                                                     DD 02-AUG-201.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match

Best Local Similarity 73.2%; Pred. No. 1.5e-21;

RESULT 1496

ID AAK81853 standard; DNA; 10248 BP.

DB Human immune/haematopoietic anti~~

PN 00-AUG-2001.

PN 00-AUG-2001.

PA (HIMA-) HUMAN GENOME SCI INC.

OUERY MATCH 1996

ID AAK81853 standard; DNA; 10248 BP.

DB Human immune/haematopoietic anti~~

PN 00-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADS36474 standard; DNA; 40947 BP.
Human autoimmune disease-related genomic DNA sequence - SEQ ID 1688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 104.4; DB 13; Length 40947; Pred. No. 3.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAK91123 standard; DNA; 14273 BP.
Human digestive system antigen genomic sequence SEQ ID NO: 4699.
WO200155314-A2.
                                                                                                                                                                                                                                                                                                                                                         Length 10248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ery Match 5.7%; Score 104.4; DB 4; Length 14273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
6-ry Match 5.7%; Score 104.4; DB 4; Length 14273;
                                                                       (HUMA-) HUMAN GENOME SCI INC.
ry Match 5.7%; Score 104.4; DB 4; Length 3683;
t Local Similarity 73.2%; Pred. No. 8.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USACUSONS.
20-MAR-2003.
20-MAR-2003.
(HUMA-) HUMAN GENOME SCI INC.
5.7%; Score 104.4; DB 9;
ery Match
5.7%; Pred. No. 1.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADB60507 standard; DNA; 10248 BP.
Connective tissue related genomic DNA #250.
US2003054375-A1.
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Best Local Similarity 7
RESULT 1497
ID ADB60507 standard; DNA
DE Connective tissue rela
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 7
RESULT 1499
ID AAK91123 standard; DNA
DE Human digestive system
PN W0200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME S
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Query Match
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Best Local Similarity
RESULT 1498
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                                                           09-AUG-2001
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A91700 Sequence
BD023443 Junction
U89915 Mus musculu
Incallo Secreted
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BD209598 Compositi
AR341404 Sequence
C0718721 Sequence
A91701 Sequence
A91701 Sequence
BD023444 Junction
A91699 Sequence
BD023442 Junction
CQ834198 Sequence
BD126359 Primer fo
AF111714 BOS tauru
AR201017 Sequence
BD080011 Human F11
BC065309 Rattus no
AF276998 Rattus no
AR276998 Rattus no
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AF241261 Rattus no
AR216156 Sequence
BC046720 Xenopus 1
BC082710 Xenopus 1
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A91702 Sequence 6
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AC087229 Mus muscu
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  Command line parameters:
-WODEL=frame+ p2n.model -DEV=xlh
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-Q=/cgn2 1/USFTO spool/US10785220/runat_07092005_161055_11753/app_query.fasta_1.455
-DB=GenEmbl -QFWT=fastap -SUFFIX=p2n.rg= -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bite -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500
-UNITS=bite -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500
-UNITS=bite -START=1 -END=-1 -MATRIX=blosum62 -TRENS=2000000000
-UNITS=bite -NONH=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-UNITS=bite -NONH=ext -HEAPSIZE=500 -MINLEN=0 -NONGENE2000000000
-UNITS=bite -NONH=ext -NON
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BD080010 Human F11
CQ834196 Sequence
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                      version 5.1.6
- 2005 Compugen Ltd.
                                                                                                                 - nucleic search, using frame_plus_p2n model
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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AX083641 Sequence BV180595 sqnm11044 BD268817 Vascular AX036060 Sequence CQ731715 Sequence AX364850 Sequence AX364850 Sequence AX364850 Sequence AX120503 Gallus ga CQ842001 Sequence AX125071 Homo sapi	CQ726679 Sequence CQ780673 Sequence CQ781567 Sequence	BD125382 Primer fo BD126276 Primer fo	AF247659 Mus muscu	AR170205 Sequence	182549 Sequence 23 BC074830 Homo sapi	BC074876 Homo sapi AR170210 Sequence	I82554 Sequence 29 BC069789 Homo sapi	BC069705 Homo sapi	BC069723 Homo sapi BC069745 Homo sapi	BC069761 Homo sapi	AX399902 Sequence CQ727019 Sequence	CQ861595 Sequence	AX330282 Sequence	AX410791 Seguence U79725 Human A33 a	AR170211 Sequence	CQ781546 Sequence	BD124855 Primer to BD126255 Primer fo	BX934867 Gallus ga	BD242048 Compounds	AR237231 Sequence	AR366951 Sequence	AR370847 Sequence	AR399987 Sequence	AR405254 Sequence	ARS63634 Sequence	AX106358 Sequence	AX200509 Sequence	AX267165 Sequence RD070284 Compounds	BD249458 Human pro	BD249468 Human pro BC007313 Homo sabi	AX056679 Sequence	AX358982 Sequence	AX362475 Sequence	BD222682 Human sig	AK000460 Homo sapi	BD233/31 31 numan Y14064 Gallus gall	Y14063 Gallus gall	BD233754 31 human	AJ306906 Homo sapi	מ
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Gupta, S.Kant. and Pillarisetti, K.
Human Fl1 antigen: a novel cell sur
platelet aggregation
Patent: US 6558707-A 1 19-MAR-2002;
Location/Qualifiers
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Fax: +49 30 32639 111

www.rzpd.de
This clone is available from RZPD;
contact RZPD (customer.service@rzpd.de) for further information.
This CDS clone is a part of a collection of human full ORF clones
generated by RZPD.
This CDS has been cloned incl. stopcodon.
The CDS has been cloned into pDONR201 via a BP Clonase(TM)
reaction. Additional sequence has been added in front of the start
codon: att. .AAAAAA GCA GGC (ATG).
After the stop codon 3' UTR sequence is present in front of the 3'
att site (ACCCAGCTTTCTT).
Compared to the reference sequence NM_144501 (gi21464106) we did
not find any amino acid exchanges.
Clone distribution: http://www.rzpd.de/products/orfclones/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / LTAIN LALL LONG "MOTTRAQVERKLLCLFILALLLCSLALGSVTVHSSEPEVR I PENN PVKLSCAYSGESSPRVEWKFDQGDTTRLVCYNNKI TASYEDRVTFLPTGITFKSVTRE DTGTYTCMVSEEGGNSYGEVKKTLI ULVPPSKRTVN I PSSATIGNRAVLITCSEDDGSPPSTYMFKDSEEGGNSYGEVKKTLI VLVPPSKRTVN I PSSATIGNRAVLITCSEDDGSPPSTYMFKOJ VMPTNYKSTRAFSNSSYVLNPTTGELVFDLISASDTGEYSCEANGY GTPMTSNAVRRAVBRAVLYVT VAAVLVTLI LLGILVFGIWFAYSRGHFDRTKKGTSSKKVI YSQPSARSEGEFKQTSSFLV"
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/db_xref="G1:49065450"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                       GAGTGGAAGTTTGACCAAGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACA
                                                                                                                                                 GCTTCCTATGAGGACCGGGTGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACA
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TTGTGCTCCCTGGCATTGGGCAGTGTTACAGTGCACTCTTCTGAACCTGAAGTCAGAATT
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Gupta, S.K. and Pillarisetti, K.
Human F11 antigen as cell surface receptor participating in
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Patent: JP 2001509312-A 1 24-JUL-2001;
SMITHKLINE BEECHAM CORP
OS HOMO Sapiens (human)
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10-JUL-1998 JP 2000502080
10-JUL-1997 US 60/052186
SHALLEY KANT GUPTA, KODANDARAM PILLARISETTI
CIZALIS/09, A61K38/00, A61K39/395, A61K45/00, A61K48/00, A61P9/00,
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Human platelet F11 receptor
Patent: US 6699688-A 1 02-MAR-2004;
Location/Qualifiers
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AR478942.1 GI:47237803
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/note="unnamed protein product"
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T cell activating gene
Patent: WO 2004058805-A 67 15-JUL-2004;
Asahi Kasei Pharma Corporation (JP)
Location/Qualifiers
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Naik, U.P., Ehrlich, Y.H. and Kornecki, E.
Mechanisms of platelet activation by a stimulatory antibody:

cross-linking of a novel platelet receptor for monoclonal antibody Pl1 with the Pc gamma RII receptor

Biochem. J. 310 (Pt 1), 155-162 (1995)
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AF207907 18-FEB-2001 Homo sapiens platelet F11 receptor mRNA, complete cds. AF207907

DEFINITION

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PVKLSCAYSGFSSPRYEWKFDQGDTTRLVCYNNKITASYEDRYTFLFGITFKSVTRE
DTGTYTCWYSEEGGANSYGEVKVKLIYLVPPSKFTYNIFSSAFIGNRAVLTCSEQDGSP
PSEYTWFKDGIVMFTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGY
GTPWTSNAYRMEAVERNVGYIVAAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSK
KVIYSQPSARSEGEFKQTSSFLV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="platelet membrane glycoprotein; monoclonal antibody F11 induces secretion and aggregation of human platelets by recognizing the F11 receptor; Method: conceptual translation with partial peptide sequencing"
                                                                                                                                                                                                                    3 (bases 1 to 1822)
Sobocka, M.B., Sobocki, T., Rushbrook, J.I., Banerjee, P., Weiss, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein id="AAF22829.1"
/db_xref="GI:6653649"
/translation="MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biology, SUNY, Health
Ave., Brooklyn, NY 11203,
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2 (bases 1 to 1822)
Sobocka,M.B., Sobocki,T., Banerjee,P., Weiss,C., Rushbrook,J.I.,
Norin,A.J., Hartwig,J., Salifu,M.O., Markell,M.S., Babinska,A.,
Bhrlich,Y.H. and Kornecki,B.
Cloning of the human platelet F11 receptor: a cell adhesion
molecule member of the immunoglobulin superfamily involved in
Blood 95 (8), 2600-2609 (2000)
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/organism="Homo sapiens"
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Submitted (19-NOV-1999) Anatomy
Science Center at Brooklyn, 450
USA
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/product="platelet F11
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/db_xref="taxon:9606"
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(C12P21/02,C12R1:645),C12N15/00,C12N5/00
CC Secreted and transmembrane polypeptides and nucleic CC acide
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CI2N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC
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              60/059122.17-SEP-1997 UG
60/059113.17-SEP-1997 UG
60/059266.15-0CT-1997 UG
60/06287.17-0CT-1997 UG
60/063846.24-0CT-1997 UG
60/063120.24-0CT-1997 UG
60/064215.52-0CT-1997 UG
60/064215.52-0CT-1997 UG
60/064216.120.24-0CT-1997 UG
60/06486.18-NOV-1997 UG
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60/066770,24-NOV-1997
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                   255
                                                                                              GCTTCCTATGAGGACCGGGTGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACA 315
                                                                                                                                                  GluValLysVallysLeulleValLeuValProProSerLysProThrValAsnIlePro 140
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                                                                                                                                                                                                                                                                        495
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                                                                              AlaSerTyrGluAspArgValThrPheLeuProThrGlyIleThrPheLysSerValThr 100
                                                                                                                                  ArgGluAspThrGlyThrTyrThrCysMetValSerGluGluGlyGlyAsnSerTyrGly 120
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CCTGAGAATAATCCTGTGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCCGTGTG 195
                            80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 1842)

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                                        CCTTCTGAATACACCTGGTTCAAAGATGGGATAGTGATGCCTACGAATCCCAAAAGCACC
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                         GluTrpLysPheAspGlnGlyAspThrThrArgLeuValCysTyrAsnAsnLysIleThr
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GENENTECH INC
OS Homo sapiens (human)
PN JP 2002223786-A/98
PD 13-AUG-2002
PP 18-DEC-2001 JP 2001385135
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JP 2002223786-A/98.
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Homo sapiens
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AUTHORS
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BD172325
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JEAN YUAN
C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC
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/organism='Homo sapiens (human)'.
Location/Qualifiers
24-OCT-1997 US 60/063120,24-OCT-1997 US 60/063120,24-OCT-1997 US 60/06329,27-OCT-1997 US 60/063329,27-OCT-1997 US 60/063329,27-OCT-1997 US 60/06356,28-OCT-1997 US 60/06356,28-OCT-1997 US 60/06356,28-OCT-1997 US 60/06356,28-OCT-1997 US 60/06374,29-OCT-1997 US 60/06374,29-OCT-1997 US 60/06374,29-OCT-1997 US 60/06374,29-OCT-1997 US 60/06372,31-OCT-1997 US 60/06372,31-OCT-1997 US 60/063870,03-NOV-1997 US 60/063870,03-NOV-1997 US 60/063870,03-NOV-1997 US 60/063870,03-NOV-1997 US 60/065846,18-NOV-1997 US 60/065846,18-NOV-1997 US 60/065870,23-NOV-1997 US 60/066772,24-NOV-1997 US 60/066772,25-NOV-1997 US 60/06772,24-NOV-1997 US 60/06772,24-NOV-19
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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BD172644
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    GCTTCCTATGAGGACCGGGTGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACA 351
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                ProLeuSerAlaSerAspThrGlyGluTyrSerCysGluAlaArgAsnGlyTyrGlyThr
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S Homo gapiens (human)

D 27-40G-2002

PF 18-DEC-2001 JP 2001385205

PR 17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059119,18-S1

17-SEP-1997 US 60/059119,18-S1

17-SEP-1997 US 60/059119,18-S1

18-SEP-1997 US 60/059266,15-OC

17-OCT-1997 US 60/059266,17-OC

21-OCT-1997 US 60/059266,17-OC

21-OCT-1997 US 60/0528786,24-OC

24-OCT-1997 US 60/0528786,24-OC
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Homo sapiens (human)
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/organism="Homo sapiens"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1842)

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     uValLysValLysLeuIleValLeuValProProSerLysProThrValAsnilePro
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18-DEC-2001 JP 2001385248
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GENEWIECH INC
OS Homo sapiens (human)
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PC C12P21/02//C12P21/08, (C12N1/19,C12R1:645), (C12N1/21,C12R1:19),
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C12N15/09,A61K45/00,A61P1/00,A61P13/12,A61P17/00,A61P17/06,
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                                                                                        TyrSerArgGlyHisPheAspArgThrLysLysGlyThrSerSerLysLysValIleTyr
CCCTGTCAGCCTCTGATACTGGAGAATACAGCTGTGGGGGCACGGAATGGGTATGGGACA
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OS Homo sapiens (human)
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PD 10-SEP-2002
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17-SEP-1997 US 60/059122,17-SEP-1997 US
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Matches:
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    /organism="Homo sapiens"
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C12N1/21, C12N5/10, C12P21/02, C12P21/08, C12Q1/02//(C12P21/08, P
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Wood, W.I., Gurney, A.L., Goddard, A., Penica, D., Chen, J. and Yuan, J. Secretory and transmembrane polypeptide and nucleic acid encoding
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CCCATGACTTCAAATGCTGTGCGCATGGAAGCTGTGGAGCGGAATGTGGGGGGTCATCGTG
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161 ProSerGluTyrThrTrpPheLysAspGlyIleValMetProThrAsnProLysSerThr 532 CTTCTGAATACACCTGGTTCAAGGTGGGATAGTGATGTCAACCCCAAGAGCACC 181 ArgAlaPheSerAsnSerSerTyrValLeuAsnProThrThrGlyGluLeuValPheAsp		RESULT 14 AR439058 LOCUS AR439058 LOCUS BETINITION Sequence 118 from patent US 6664376. ACCESSION AR439058.1 GI:42664907 KEYWORDS SOURCE ORGANISM Unknown. Unclassified. REFERENCE 1 (bases 1 to 1857) AUTHORS Ashkenazi,A., Botstein,D., Desnoyers,L., Eaton,D.L., Ferrara,N.,	Filvarofif, F., Fong, NQ., Gerber, H., Gertresen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Hillan, K.J., Kljavin, L.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A., Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I. Secreted and transmembrane polypeptides and nucleic acids encoding the same JOURNAL Patent: US 6664376-A 118 16-DEC-2003; FEATURES 1. 1857 Source   Location/Qualifiers Source   Vorganism="unknown"   Mol_type="genomic DNA"	Alignment Scores: 2.24e-127 Length: 1857 Pred. No.: 1544.00 Matches: 299 Score: 1544.00 Matches: 0 Percent Similarity: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Ouery Match: 6 Gaps: 0	US-10-785-220B-1 (1-299) x AR439058 (1-1857)  Qy
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172 CCTGAGAATAATCCTGTGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTG 231 61 GluTrpLy8PheAspGlnGlyAspThrThrArgLeuValCysTyrAsnAsnLy8IleThr 80 61 HIIITHIIIHIIIHIIIHIIHIHIHIHIHIHIHIHIHIH	AlaSerTyrGluAspArgValThrPheLeuProThrGly1leThrPheLysSerValThr	GCTICCTATGAGGGCCGGGGTGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGGTGACA ArgGluAspThrGlyThrTyrThrCysMetValSerGluGluGlyGlyAsnSerTyrGly	352 CGGGAAGACACTGGGACATACACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGG 411 121 GluValLysValLysLeuIleValLeuValProProSerLysProThrValAsnIlePro 140	412 GAGSTCAAGSTCAAGSTCAAGSTGAGSTTAGTGSTTAGTGSTTAGTGST 471 141 SerSerAlaThrIleGlyAenArgAlaValLeuThrCysSerGluGlnAspGlySerPro 160	472 TCCTCTGCCACCATTGGGAACCGGGCAGTGCTGACATGCTCAGAACAAGATGGTTCCCCA 531 161 ProSerGluTvrThrTrpPheLveAspGlvIleValWetProThrAspProLvsSerThr 180		181 ArgalaPheSerAsnSerSerTyrValLeuAsnProThrThrGlyGluLeuValPheAsp 200	201 ProLeuSeralaSeraspThrGlyGluTyrSerCysGlualaArgAsnGlyTyrGlyThr 220	221 PrometThrSerAsnAlaValArgMetGluAlaValGluArgAsnValGlyVallleVal 240	241 AlaAlaValLeuValThrLeuIleLeuLeuGlyIleLeuValPheGlyIleTrpPheAla 260	261 TyrSerArgGlyHisPheAspArgThrLysLysGlyThrSerSerLysLysLysVallleTyr 280		AR473078 1857 bp DNA linear PAT 20-FEB-2004 Sequence 118 from patent US 6686451. AR473078 AR473078.1 GI:42708453				ce 1. 185/ /organism="unknown" /mol_type="genomic DNA"
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Score: 1544.00 Percent Similarity: 100.00\$ Best Local Similarity: 100.00\$ Query Match: 4	US-10-785-220B-1 (1-299) x US-09-39 Oy 1 MetGlyThrLysAlaGlnVal	16	Db 76 TIGHGERCAGGGCATTGGGC	41	Oy 61 GluTrpLysPheAspGlnGly	Db 196 GACTGGAGATTTCACCACACACACACACACACACACACAC	256	OY 101 AFGGLASPURKELYINTTYTY DD 316 CGGGAAGACACTGGGACATAC	Oy 121 GluValLysValLysLeuIle'	Db 376 GAGGTCAAGGTCAAGCTCATCI			Db 496 CCTTCTGAATACACCTGGTTC. Qy 181 ArgAlaPheSerAsnSerSer	556	Oy 201 ProLeuSerAlaSerAspThr0	221	Db 676 CCCATGACTTCAAATGCTGTG	Oy 241 AlaAlaValLeuValThrLeu	Db 736 GCAGCCGTCCTTGTAACCCTG	261	796	Db 856 AGCCAGCCTAGTGCCCGAAGT	RESULT 3 US-09-907-794A-118	; Patent No. 6635468 ; GENERAL INFORMATION:
Db 284 CCTGAGAATAATCCTGTGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTG 343  Qy 61 GluTrpLysPheAspGlnGlyAspThrThrArgLeuValCysTyrAsnAsnAsnLys1leThr 80	Qy 81 AlaSerTyrGluAspArgValThrPheLeuProThrGlylleThrPheLysSerValThr 100 	101 ArgGluAspThrGlyThrTyrThrCy8MetValSerGluGluGlyGlyAsnSerTyrGly	DD 464 GGGGAAGACACTGGGACATACACTTGTATGGTCTCTGAGGAAGGGGGCGACAAGGTATGGG 523 Qy 121 GluValLysValLysGeuIleValLeuValProProSerLysProThrValAsnIlePro 140	524 GAGGTCAAGGTCAAGGTCAAGGTTGTTTTTTTTTTTTTT	OY 141 SEISETALATHITTEGEAACHGALAWILDELTHIC VESEIGLUGINASDELYSGEFIO LEU	Oy 161 ProSerGluTyrThrTrpPheLysAspClyIleValMetProThrAsnBroLysSerThr 180	181 ArgAlaPheSerAenSerSerTyrValLeudsnProThrThrGlyGluLeuValPheAsp	DB 704 CG1GCCTTCAGCAACTCTTCCTATGTCCCACAACTCCCACAAGAGGGGGGGG	Db 764 CCCTGTCAGCCTCTGATACTGGAGAATACAGCTGTGAGGGACAGGGAATGGGTATGGGACA 823	Oy 221 ProMetThrSerAsnalaValArgMetGluAlaValGluArgAsnValGlyValIleVal 240	241 AlaAlaValLeuValThrLeuIleLeuLeuGlyIleLeuValPheGlyIleTrpPheAla	884 GCAGCGTCTTTGTAACCCTGATTCTTGGGAATCTTGGTTTTTGGCATCTTGGTTTTGC	Oy 261 TyrserArgolyHisbheAspArgThrLysLysGlyThrSerSerLysLysVall1ETyr 280 	281 SerGlnProSerAlaArgSerGluGlyGluPheLysGlnThrSerSerPheLeuVal	CCAGCC	US-09-397-243D-1 ; Sequence 1, Application US/09397243D	; Falent NO. 0039000 ; GENERAL INFORMATION: ; ADDITCANT Kornecki Rlizabeth	, APPLICANT: NOTICE, MAIGOTZATA B. ; TITLE OF INVENTION: Human Platelet F11 Receptor	97.2		; PRIOR FILING DATE: 1998-09-16 ; NUMBER OF SEQ ID NOS: 27	; SOFTWAKE: Facencin ver. 2.1 ; SEQ ID NO 1 ; LENGTH: 1822	; life: DNA ; ORGANISM: Homo sapiens US-09-397-243D-1	Alignment Scores: , Pred. No.: 2.06e-176 Length: 1822

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yServalThrValHisSerSerGluProGluValArgile 40
                                                                                                                                                                                                                                        1ThrPheLeuProThrGly1leThrPheLysSerValThr 100
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                                                                                                                                                                                                                                                                                                                        eValLeuValProProSerLysProThrValAsnIlePro 140
                                                                                                                                                                                                                                                                                                                                                               nArgAlaValLeuThrCysSerGluGlnAspGlySerPro 160
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                                                                                                                                                            yAspThrThrArgLeuValCysTyrAsnAsnLysIleThr 80
                                                                             rGluGlyGluPheLysGlnThrSerSerPheLeuVal 299
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Matches:
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121 GluValLysValLysLeuIleValLeuValProProSerLysProThrValAsnIlePro 140
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PELLING DATE: 1999-07-26

PRIOR PELLING DATE: 1999-07-26

PRIOR PELLING DATE: 1999-07-26

PRIOR PELLING DATE: 1999-07-26

PRIOR PELLING DATE: 1999-07-36

PRIOR PELLING DATE: 1999-07-15

PRIOR PELLING DATE: 1999-01-15

PRIOR APPLICATION NUMBER: PCT/US99/2814

PRIOR APPLICATION NUMBER: PCT/US99/2814

PRIOR APPLICATION NUMBER: PCT/US99/2814

PRIOR APPLICATION NUMBER: PCT/US99/2814

PRIOR PELLING DATE: 1999-11-30

PRIOR PELLING DATE: 1999-12-02

PRIOR PELLING DATE: 1999-12-03

PRIOR PELLING DATE: 199
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Grimaldi, Christopher
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Wood, William, I.
                                                                                                                            Ferrara, Napoleone
Filvaroff, Ellen
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Gerber, Hanspeter
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Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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; ORGANISM: Homo
US-09-907-794A-118
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APPLICANT:
APPLICANT:
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411

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; Sequence 118, Application US/09905125A; Patent No. 6664376; GENERAL INFORMATION:
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Alignment Scores: Pred. No.:

240

220

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Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14 Same
FILE REPERENCE: 10466-14 Same
FILE REPERENCE: 10466-14 Same
CURRENT FILING DATE: 2000-07-12

### PRIOR PELLING DATE: 2000-07-22

### PRIOR APPLICATION NUMBER: US 60/145,698

### RIOR PILING DATE: 1999-07-78

### RIOR PELLING DATE: 1999-07-38

### RIOR PELLING DATE: 1999-09-13

### RIOR PELLING DATE: 1999-10-13

### RIOR REPLICATION NUMBER: PCT/US99/28313

### RIOR APPLICATION NUMBER: PCT/US99/28313

### RIOR PELLING DATE: 1999-11-20

### RIOR PELLING DATE: 1999-12-02

### RIOR PELLING DATE: 1999-12-03

### RIOR PELLING DATE: 1999-1
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Grimaldi, Christopher
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc.
Eston, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
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Williams, P. Mickey
Wood, William, I.
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Gao, Wei-Qiang
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US-09-905-125A-118
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Length

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241 AlaAlaValLeuValThrLeuIleLeuLeuGlyIleLeuValPheGlyIleTrpPheAla 260
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US-09-902-775A-118
Sequence 118, Application US/09902775A
Patent No. 6686451
GENERAL INFORMATION:
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101 ArgGluAspThrGlyThrTyrThrCysMetValSerGluGluGlyGlyAsnSerTyrGly 120
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     Matches:
Conservative:
Mismatches:
Indels:
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              Percent Similarity:
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Query Match:
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APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/902,775A

CURRENT APPLICATION NUMBER: US/09/902,775A

CURRENT APPLICATION NUMBER: US/09/902,775A

CURRENT APPLICATION NUMBER: PCT/US00/04414

PRIOR PILING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-08

PRIOR PLING DATE: 1999-07-08

PRIOR PLING DATE: 1999-09-08

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PRIOR PLING DATE: 1999-09-13

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PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-11-20

PRIOR PPLICATION NUMBER: PCT/US99/2091

PRIOR PLING DATE: 1999-12-02

PRIOR PPLICATION NUMBER: PCT/US99/30099

PRIOR PLING DATE: 1999-12-16

PRIOR PLING DATE: 1999-12-16

PRIOR PLING DATE: 1999-12-06

PRIOR PLING DATE: 1999-12-07

PRIOR PLING DATE: 1999-12-06

PRIOR PLING DATE: 199
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Godowski, Paul J.
Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
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Paoni, Nicholas F.
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Gerber, Hanspeter
Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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ORGANISM: Homo sapiens
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US-09-906-700-118
; Sequence 118, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:

240

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Length:

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Alignment Scores: Pred. No.:

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Percent Similarity:
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Query Match:
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APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ACLOS ELECOLDING THE SAGINE CURRENT APPLICATION NUMBER: US/09/906,700 CURRENT FILING DATE: 2000-09-18 PRIOR APPLICATION NUMBER: PCT/USOO/04114 PRIOR APPLICATION NUMBER: PCT/USOO/04114 PRIOR PILING DATE: 1990-07-26 PRIOR FILING DATE: 1990-07-26 PRIOR FILING DATE: 1990-07-26 PRIOR FILING DATE: 1990-07-26 PRIOR FILING DATE: 1990-07-26 PRIOR PILING DATE: 1990-07-26 PRIOR PILING DATE: 1990-07-26 PRIOR PILING DATE: 1990-09-18 PRIOR PILING DATE: 1990-09-18 PRIOR PILING DATE: 1990-09-18 PRIOR PILING DATE: 1990-09-18 PRIOR PILING DATE: 1990-09-15 PRIOR PILING DATE: 1990-01-15 PRIOR PILING DATE: 1990-01-15 PRIOR PILING DATE: 1990-01-15 PRIOR PILING DATE: 1990-10-05 PRIOR PILING DATE: 1990-11-29 PRIOR PILING DATE: 1990-11-29 PRIOR PILING DATE: 1990-11-29 PRIOR PILING DATE: 1990-12-02 PRIOR PILING DATE: 1990-12-02 PRIOR PILING DATE: 1990-12-02 PRIOR PILING DATE: 1990-12-07 PRIOR 
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Grimaldi, Christopher
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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Length:

2.12e-176

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AlaserTyrGluAspArgValThrPheLeuProThrGly11eThrPheLysSerValThr 100
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                Conservative:
Mismatches:
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US-09-903-603A-118
Sequence 118, Application US/09903603A
Parent No. 676/995
GENERAL INFORMATION:
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TITLE OF INVENTION: Secret ed and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secret ed and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/09/03,603A
PRIOR APPLICATION NUMBER: US/01/14,048
PRIOR APPLICATION NUMBER: US/01/14,048
PRIOR APPLICATION NUMBER: US/01/14,048
PRIOR APPLICATION NUMBER: US/01/14,222
PRIOR PLILNG DATE: 1999-07-0.26
PRIOR PLILNG DATE: 1999-01-1.20
PRIOR APPLICATION NUMBER: PCT/US99/28014
PRIOR APPLICATION NUMBER: PCT/US99/28014
PRIOR APPLICATION NUMBER: PCT/US99/28014
PRIOR APPLICATION NUMBER: PCT/US99/28014
PRIOR APPLICATION NUMBER: PCT/US99/28056
PRIOR APPLICATION NUMBER: PCT/US99/28056
PRIOR PRILNG DATE: 1999-11-0.05
PRIOR PLILNG DATE: 1999-11-0.05
PRIOR PLILNG DATE: 1999-12-0.2
PRIOR PLILNG DATE: 1999-12-0.3
PRIOR PRING DATE: 1999-12-0.3
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Grimaldi, Christopher
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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                                                                              Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
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Stewart, Timothy A.
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Gerber, Hanspeter
Gerritsen, Mary E.
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Paoni, Nicholas F
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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; ORGANISM: Homo sapiens
US-09-903-603A-118
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                                                                                                                                                                                                                                                                                                                                                                       41 ProGluAsnAsnProValLysLeuSerCysAlaTyrSerGlyPheSerProArgVal
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                                                                                                                                       US-10-785-220B-1 (1-299) x US-09-903-603A-118 (1-1857)
Matches:
Conservative:
Mismatches:
Indels:
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Query Match:
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APPLICANT: William, I.
APPLICANT: World william, I.
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Mucleic
ITILE OF INVENTION: Acids Encoding the Same
TITILE OF INVENTION: Acids Encoding the Same
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TITILE OF INVENTION: Acids Encoding the Same
CURRENT PRINCE APPLICATION MUMBER: US/09/904,920A
CURRENT FILING DATE: 2000-02-20A
FRIOR APPLICATION NUMBER: PCT/US00/0414
FRIOR PILING DATE: 1999-07-26
FRIOR APPLICATION NUMBER: PCT/US99/20594
FRIOR PILING DATE: 1999-07-26
FRIOR APPLICATION NUMBER: PCT/US99/20594
FRIOR PILING DATE: 1999-09-16
FRIOR PILING DATE: 1999-09-16
FRIOR APPLICATION NUMBER: PCT/US99/20594
FRIOR PILING DATE: 1999-09-16
FRIOR PILING DATE: 1999-09-16
FRIOR PILING DATE: 1999-09-15
FRIOR PILING DATE: 1999-09-15
FRIOR PELLING DATE: 1999-09-15
FRIOR PILING DATE: 1999-09-15
FRIOR PILING DATE: 1999-11-30
FRIOR PAPILCATION NUMBER: PCT/US99/3099
FRIOR P
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Grimaldi, Christopher
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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Goddard, A.
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CRGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                 CCTGAGAATAATCCTGTGAAGTTGTCCTGTGCCTACTCGGGCTTTTTCTTCTCCCCGTGTG
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                                                                                                                                                                             1 MetGlyThrLysAlaGlnValGluArgLysLeuLeuCysLeuPhelleLeuAlaIleLeu
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Conservative:
Mismatches:
Indels:
                                                                                                                                 US-10-785-220B-1 (1-299) x US-09-904-920A-118 (1-1857)
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; Sequence 118, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
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100.00%
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Conservative: Mismatches: Indels:

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Matches:

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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## APPLICANT: Williams, Daniel
## APPLICANT: Williams, Wi
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Godowski, Paul J.
Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
                                                                                                                                                                                                                                                                                                                                                Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
           Ashkenazi, Avi
Botsetin, David
Desnoyers, Luc
Baton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
                                                                                                                                         Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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ORGANISM: HOMO
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Alignment Scores: Pred. No.:

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AlaSerTyrGluAspArgValThrPheLeuProThrGlyIleThrPheLysSerValThr 100
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US-10-785-220B-1 (1-299) x US-09-909-064-118 (1-1857)
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221 ProMetThrSerAsnAlaValArgMetGluAlaValGluArgAsnValGlyValIleVal 240
                                                                                                                                                                              AlaSerTyrGluAspArgValThrPheLeuProThrGlyIleThrPheLysSerValThr 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              472 recrereceaceatregaaaceegecagrecreacarecreagaacaagaregrieceea 531
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                                                                                                                                     US-10-785-220B-1 (1-299) x US-09-905-381A-118 (1-1857)
      Matches:
Conservative:
Mismatches:
Indels:
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      1544.00
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rercent Similarity:
Best Local Similarity: ;
Query Match:
DB:
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APPLICANT: Kijavin, Vasineui, J.
APPLICANT: Kijavin, Vasineui, J.
APPLICANT: Macher, Jennie P.
APPLICANT: Pan, James P.
APPLICANT: Pan, James P.
APPLICANT: Pan, James P.
APPLICANT: Pan, James P.
APPLICANT: Pool, William, I.
IIIama, P. William, I.
IIIIam, I.
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IIIII OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIII.
IIII OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIIII OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIII.
IIII OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIII.
IIII OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIII.
IIII OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIII.
IIII OF INVENTION NUMBER: US 60/143, 048
PRIOR FILING DATE: 1999-0-22
PRIOR FILING DATE: 1999-0-12
PRIOR FILING DATE: 1999-0-12
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-14
PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-11-17
PRIOR FILING DATE: 199
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Grimaldi, Christopher
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                       Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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                                                                                                                                                                                                    Gerber, Hanspeter
        Genentech, Inc.
Ashkenazi, Avi
Botstein, David
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Gao, Wei-Qiang
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JS-09-905-381A-118
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651

591

220

711

1857

Length:

2.12e-176

Alignment Scores: Pred. No.:

Matches: Conservative: Mismatches: Indels:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ## APPLICANT: Tunnas, Daniel
## APPLICANT: Williams, P. Mickey
## APPLICANT: Wood, William, I.
## TITLE OF INVENTION: Acids Encoding the Same
## CURRENT PILING DATE: 2001-07-16
## PRIOR PILING DATE: 2000-07-16
## PRIOR APPLICATION NUMBER: US 60/145,698
## PRIOR APPLICATION NUMBER: US 60/146,222
## PRIOR PILING DATE: 1999-07-28
## PRIOR PILING DATE: 1999-01-38
## PRIOR PILING DATE: 1999-01-38
## PRIOR PILING DATE: 1999-10-38
## PRIOR PILING DATE: 1999-10-39
## PRIOR PILING DATE: 1999-10-39
## PRIOR PILING DATE: 1999-10-39
## PRIOR PILING DATE: 1999-10-30
## PRIOR PI
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Grimaldi, Christopher
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
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Gerber, Hanspeter
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Goddard, A.
Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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; ORGANISM: HOMO
US-09-906-618-118
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1857

Length:

2.12e-176

Alignment Scores: Pred. No.:

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                                                                                                                                                                                                                                                                                                                               LeuCysSerLeuAlaLeuGlySerValThrValHisSerSerGluProGluValArgile
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TyrSerArgGlyHisPheAspArgThrLysLysGlyThrSerSerLysLysVallleTyr 280
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                                             241 AlaAlaValLeuValThrLeuIleLeuGlyIleLeuValPheGlyIleTrpPheAla
                                                                796 GCAGCCGTCCTTGTAACCCTGATTCTCCCTGGGAATCTTGGTTTTTGGCATCTGGTTTGCC
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Matches:
Conservative:
Mismatches:
Indels:
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Sequence 254, Application US/09312283C
Sequence 254, Application US/09312283C
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Reme G.
APPLICANT: Murison, James G.
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT APPLICATION NUMBER: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FRASESEQ for Windows Version 4.0
SEQ ID NO 254
LENGTH: 1421
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Best Local Similarity:
Query Match:
DB:
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US-09-312-283C-254
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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matchew
APPLICANT: Sleeman, Matchew
APPLICANT: Ontue! Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: Land Methods For Their Use
FILE REPERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 254
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  LeuCysSerLeuAlaLeuGlySerValThrValHisSerSerGluProGluValArgIle
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Sequence 70, Application US/09312283C

Sequence 70, Application US/09312283C

SERNERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Sleeman, Matthew
APPLICANT: OSTERNIA, Rene
APPLICANT: Murison, James G.

WINGER OF SEQ ID NOS: 425
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GluValLysValLysLeulleValLeuValProProSerLysProThrValAsnIlePro
                                                       SerSerAlaThrIleGlyAsnArgAlaValLeuThrCysSerGluGlnAspGlySerPro
                                                                                                                                                                      ArgAlaPheSerAsnSerTyrValLeuAsnProThrThrGlyGluLeuValPheAsp
                                                                                                                                                                                                                                                                                                                                                                                                                      496 TCCTCTGCCACCATTGGGAACCGGGCAGTGCTGACATGCTCAGAACAAGATGGTTCCCCA
                                                                                                                                                                                                   616 cerecerreageaacrerrecrarerecreaarcecacaacagagagererrraar
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Patent No. 6150502

GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: Compositions Sor Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348

SOFTWARE: FaetSEQ for Windows Version 3.0
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Matches:
Conservative:
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; ORGANISM: Human
US-09-188-930-70
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US-09-188-930-70
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TyrSerArgGlyHisPheAspArgThrLysLysGlyThrSerSerLysLysValIleTyr 280
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; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 70; LENGTH: 1421; TYPE: DNA AUGUST OF SORGANISM: Mouse US-09-312-283C-70
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US200317158-A1.
                                                                                                                                                                                                                                                                                                                                                ADK40842 standard; cDNA; 1822 BP.
DNA encoding human platelet F11 receptor #1
US6699688-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADR27640 standard; cDNA; 1822 BP.
Full length human F11 receptor cDNA Seq 6.
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Human cDNA clone DNA40628 encoding PRO301.
WO9914241-A2.
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(UTNY ) UNIV NEW YORK STATE RES FOUND.
IL Similarity: 100.00% Mism
Local Similarity: 100.00% Mism
Match: Match: Index
                                                                                                                         Human polynucleotide SEQ ID NO 1261.
                                (ASAH-) ASAHI KASEI PHARMA CORP.
Ent Similarity: 100.003
Local Similarity: 100.003
Match: 100.003
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                                                                                                                                       ABL90699 standard, Carlo B Human polymuclectide SEQ ID NO 10 PN WC200190304-A2.

PN WC200190304-A2.

PD 29-NOV-2001. $\pi$
PA (HUMA-) HUVAN GENOME SCI INC.
Percent Similarity: 100.00$

Best Local Similarity: 100.00$
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PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
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NAPIER M A.
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DE DNA encoding hum
VS669968-B1.
PD 02-WAR-2004.
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RESULT 7
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RESULT 9
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OM protein - nucleic search, using frame plus p2n model

Run on: September 8, 2005, 20:54:18 ; Search time 638 Seconds

(without alignments)

2774.299 Million cell updates/sec
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WO2003008541-A2.
30-JAN-2003.
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 4390206 segs, 2959870667 residues
Total number of hits satisfying chosen parameters:
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Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum March 100%
Listing first 1500 summaries
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Percent Similarity: Best Local Similarity: Query Match:	RESULT.  ID ADN35294 standard;  DE Human PRO301 gene D  N W02004031105-A2.  PD 15-ARR-2004.  PA (GETH ) GENENTECH I  Percent Similarity:  Query Match:	RESULT 12 LD ADRIL1005 standard; CDNA; 1850 DE Human secreted/transmembrane PN US2004137561-Al.	PD 15-JUL-2004.  PA (GETH ) GENENTECH I Percent Similarity: Best Local Similarity: Query Match:	KESULI 13 ID AAZS2204 standard; CDNA; 1857 DE Human PRO301 protein encoding PN WO200015797-A2.	PD 23-MAR-2000.  PA (GETH ) GENENTECH I Percent Similarity: Best Local Similarity:	ALSO AAA77581 standard; ID AAA77581 standard; DE Human PRO301 CDNA s PN WO200032221-A2.	000. GENENTECH arity: milarity:	KESULT 15 ID AAA49723 standard; DE Human PRO301 cDNA c PN WO200037638-A2.	PD 29-JUN-2000. PA (GETH) GENENTECH I Percent Similarity: Best Local Similarity: Query Match:	RESOLI 16 TD ADC78438 standard; DE Human PRO301 cDNA. PN WO200015796-A2.	000. GENENTECH arity: milarity:	DE Human PRO301 cDNA.  WOODOOLOGE	PD 18-JAN-2011. PA (GETH ) GENENTECH I Percent Similarity: Query Match:	RESULT 15  AAC87026 standard; CD  DE Nucleotide sequence o  PN W020077037-A2.  PD 21-DEC-2000.  PA (GETH) GENENTECH INC

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and	INC. 100.00\$ 100.00\$ 100.00\$	; cDNA; 1857 BP. an PRO polypeptide	INC. 100.00% 100.00% 100.00%	; cDNA; 1857 BP ng secreted/tra	INC. 100.00% 100.00% 100.00%		INC. 100.00% 100.00% 100.00%	; cDNA; 1857 BP ansmembrane pol	INC. 100.00\$ 100.00\$ 100.00\$	cDNA; 1857 B secreted and	INC. 100.00\$ 100.00\$ 100.00\$	; cDNA; 1857 BP ansmembrane pro	INC. 100.00% 100.00% 100.00%	; cDNA; 1857 BP ansmembrane pro	INC. 100.00% 100.00% 100.00%	
DE Novel human secreted	PD 26-DEC-2002. PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	15	PD 20-FEB-2003. PA (GETH ) GENENTECH PETCENT Similarity: Best Local Similarity: Query Match:	RESULT 27 ID ABX71545 standard; CDNA; 1857 BP. DE Human CDNA encoding secreted/transmembrane PN US2002132240-A1.	PD 19-SEP-2002. PA (GETH ) GENENTECH PERCENT Similarity: Best Local Similarity: Query Match:	RESULT 28 ID ACAO4985 standard; CDNA; DE Novel human secreted and PN US2003032063-A1. DN 13-EFB-2003	GENENTECH arity: milarity:	KESULT 29  ID ACHO6877 standard; cDNA; 1857 BP. DE Human secreted/transmembrane polypeptide	PN 052003044835-A1. PD 06-MAR-2003. PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	5	PD 23-JAN-2003. PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	RESOLI 31  ID ACD1977 standard; CDNA; 1857 BP.  DE Human secreted/transmembrane protein PN US2003036179-Al.	PD 20-PEB-2003. PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	4 standard ecreted/tr 60374-A1.	PD 31-OCT-2002. PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	RESULT 33 ID ACA60515 standard; cDNA; DE Novel human secreted and

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Human cDNA encoding a secreted/transmembrane protein, SEQ ID 365.
US2003032155-A1.
13-FEB-2003.
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Novel human secreted and transmembrane protein PRO301 cDNA.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003022328-A1.
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Novel human secreted and transmembrane protein PRO301 DNA.

NY S2003032062-A1.

NY (GETH) GENERYECH INC.

Percent Similarity: 100.00$ Conservative: 0

Sest Local Similarity: 100.00$ Mismatches: 0

Duery Match: 100.00$ Indels: 0
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97 9203030257-A1.
98 13-FEB-2003.
94 (GETH ) GENENTECH INC.
98 CORSET Similarity: 100.00% Conservative: 0 Secret Local Similarity: 100.00% Mismatches: 0 Duery Match: 0
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Human secreted / transmembrane polypeptide PRO301 cDNA.
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20-FBB-2003.
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US2003023054-Al.
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ESULT 39
D ACA65646 standard; cDNA; 1857 BP.
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PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
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HESULY St. Human secreted/transmembrane protein CDNA, #25.

Pub (S2003039971-A1.

Pub (S2003039971-A1.

Pub 27-FEB-2003.

Pub (GETH) CENENTECH INC.

Percent Similarity: 100.00$ Mismatches: 0

Query Match: 100.00$ Mismatches: 0

RESULY S3

ID ACD66887 standard; CDNA, 1857 BP.

Pub (GETH) CENENTECH INC.

Pub (GETH) CENENTECH INC.

Pub (GETH) CENENTECH INC.

Pub (GETH) CENENTECH INC.

Percent Similarity: 100.00$ Mismatches: 0

Percent Similarity: 100.00$ Mismatches: 0

RESULY S3

ID ADA67538 standard; CDNA, 1857 BP.

Percent Similarity: 100.00$ Mismatches: 0

Query Match: 100.00$ Mismatches: 0

Percent Similarity: 100.00$ Mismatches: 0

Query Match: 100.00$ Mismatches: 0

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RESULT 55

ID ADA65841 standard; CDNA; 1857 BP.

DE Novel human secreted and transmembrane protein PRO301 CDNA.

PN US2003082693-A1.

PD 01-MAY-2003.

PA (GETH ) GENENTECH INC.

Percent Similarity: 100.00$ Conservative: 0

Best Local Similarity: 100.00$ Mismatches: 0

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DE Human PRO polynucleotide #183.
PN US2003082705-Al.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
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PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH ) GENEWIECH INC.
Percent Similarity: 100.00%
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DE Human PR
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Query Match:	1211 standard; 1 PRO polynucl 13073216-A1. 18-2003.	ğ # ğ	RESULT 75  ID ADA82289 standard; cDNA; 1857 BP.  DE Novel human secreted and transmembrane protein PRO301  PN US2003082695-A1.	PA (GETH) GENENTECH INC. Percent Similarity: 100 Best Local Similarity: 100 Query Match: 100	RESULT 76  DD ADA84737 standard; cDNA; 1857 BP.  DE Novel human secreted and transmembrane protein PRO301  PN US2003082708-A1.	01-MAY-2003. (GETH) GENENTECH ccent Similarity: it Local Similarity: rry Match:	ACD2126 standard; cDNA; DE Human PRO polynucleotide PN US2003064367-A1. PD 03-APR-2003.	cent Simi	RESOLI 78 ID ADB29993 standard; cDNA; 1857 BP. DE CDNA encoding human PRO polypeptide #183 PN US2003073214-A1.	PD 17-APR-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 100 Best Local Similarity: 100 Query Match: 100	RESOLI /95 BP ID ADA80521 standard; cDNA; 1857 BP DE Human PRO polynucleotide #183. PN US2003082761-A1. PD 01-MXY-2003	PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Query Match:		PA (GETH ) GENENTECH INC Percent Similarity: 100 Best Local Similarity: 100 Query Match: 100	RESOLT 81  ID ADA46988 standard; CDNA; DE Human PRO polynucleotide PN US2003073210-A1. PD 17-APR-2003. PA (GETH) GENENTECH INC. Percent Similarity: 100.00 Best Local Similarity: 100.00	Query Match:

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ADB21743 standard; cDNA; 1857 BP.
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         ADA95949 standard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
US2003082759-A1.
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ID ADA95949 standard; cura, constitution and properties and proper
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Novel human secreted and transmembrane protein PRO301 CDNA.
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US2003054516-A1.
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    Human secreted/transmembrane protein cDNA, #25.
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ID ADB28466 standard; CDNA; 1857 BP.
DE CDNA encoding human PRO polypeptide #183.
PN US2003082699-A1.
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US2003082706-Al.
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ID ADA17222 standard; cDNA; 1857 BP.
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ID ADB29018 standard; cDNA; 1857 BP
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DE Human secreted/trans
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FN 022030/5215-A1. PD 17-ARR-2003. PA (GETH) GENENTECH: Percent Similarity: Best Local Similarity: Query Match:	S standard RO polynuc 82686-A1. 2003. GENENTECH larity: imilarity:	TENDAL 1987 BP.  ID ADB27362 standard; CDNA; 1857 BP.  DE CDNA encoding human PRO polypeptide PN US2003022239-Al.  PD 30-JAN-2003.  Percent Similarity: 100.00% Mi Best Local Similarity: 100.00% Mi COURTY MATCH: 100.00% IN	DE ADB22295 standard; cDNA; 1857 BP. DE Novel human secreted and transmembrane protopy US2003087344A1. PD 08-MAY-2003.	Percent Similarity: Best Local Similarity: Query Match:	KESULI 110 ID ACD30262 standard; cDNA; 1 DE Human cDNA encoding Pro302 PN US2003044902-Al.		ID ACD23588 standard; cDNA; DE Human PRO polynucleotide PN US2003064922-A1. PD 03-APR-2003. PA (GETH ) GENENTECH INC. POFFCEL SIMILATILY: 100.00	Query Match: 100.00% RESULT 112 ID ADA66986 standard; CDNA; 1857 DE Human PRO polynucleotide #183	PN USZUGGB193-AL. PD 10-APR-2003. PA (GETH) GENENTECH Percent Similarity: Best Local Similarity:	RESULT 113 ID ADB22847 standard; cDNA; DE Human PRO polynucleotide PN US20030777711-A1. PD 24-APR-2003	PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Ouery Match:	ID ADB23620 standard; cDNA; 1857 BP. DE Human PRO polynucleotide SEQ ID NO PO USECCIÓN SEQ SEQ DE NO PD 24-APR-2003.

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DB38657 standard; cDNA; 1857 BP.
ovel human secreted and transmembrane protein PRO301 cDNA.
32003082766-A1.
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90'vel human secreted and transmembrane protein PRO301 CDNA.

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GETH ) GENENTECH INC.

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Ap92342 standard; cDNA; 1857 BP.
vvel human secreted and transmembrane protein PRO301 cDNA.
32003082712-A1.
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ovel human secreted and transmembrane protein PRO301 cDNA.
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tuman secreted/transmembrane protein CDNA, #25.
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uman PRO polynucleotide #183.
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Novel human secreted and transmembrane protein PRO301 cDNA. US2003092106-A1.
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Novel human secreted and transmembrane protein PRO301 CDNA.
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          ADC29319 standard; cDNA; 1857 BP.
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US2003049676-Al.
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Human secreted/transmembrane protein cDNA, #25.
US2003073079-A1.
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US2003049677-A1.
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Human secreted/transmembrane protein cDNA, #25.
US2003054400-Al.
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US2003054441-A1.
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ADC33840 standard; cDNA; 1857 BP
      DE Human secreted/transmembrane p
PN 42203049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
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PD 17-APR-2003.
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PN US2003073079-A1.
PD 17-APR-2003.
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PD 15-MAY-2003.
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DE Novel human secreted and tran-
PN US2003092107-A1.
PD 15-MAY-2003.
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PN US200305400-A1.
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RESULT 143
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ADC57293 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein cDNA Seq ID365.
US2003087366-A1.
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RESULT 153

ADC54584 standard; CDNA; 1857 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID365.
PN US2003087363-A1.
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Novel human secreted and transmembrane protein cDNA Seq ID365.
US2003087364-A1.
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US2003087365-A1.
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ID ADCS0959 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003087361-A1.
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  ADC59932 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003092105-A1.
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ID ADC59068 standard; cDNA; 1857 BP
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ADC52939 standard; cDNA; 1857 BP
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ID ADC59932 standard, ....., DB Novel human secreted and trans by US2003092105-A1.
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ID ADC65486 standard;
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US2003194776-A1.
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Novel human secreted and transmembrane protein cDNA Seq ID365.
US20030871360-A1.

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(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein cDNA Seq ID365.
US2003087346-A1.
08-MAY-2003.
 Novel human secreted and transmembrane protein cDNA Seg ID365.
US2003087359-A1.
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(GETH ) GENENTECH INC.
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Wovel human secreted and transmembrane protein PRO301 cDNA.
US2003091104-A1.
15-MAY-2003.
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Novel human secreted and transmembrane protein PRO301 CDNA.
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CONA encoding human PRO polypeptide #183.
US2003194770-A1.
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Human PRO polynucleotide #183.
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Human PRO polynucleotide #183.
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(GETH ) GENENTECH INC.
DE Novel human secreted PN US2003087359-A1. PD 08-MAY-2003. PA (GETH) GENETECH IN Percent Similarity: 18est Local Similarity: 10cery Match:
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ADD04594 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003087354-Al.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003092103-A1.
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US2003105011-A1.
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Human secreted/transmembrane protein cDNA, #25
US2003104469-Al.
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US200319471-A1.
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US2003194774-A1.
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(GETH ) GENENTECH INC.
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RESULT 166
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1 INC. 100.00% : 100.00% 100.00%	d; cDNA; 1857 BP clectide #183. H INC. 100.00\$ 100.00\$	<pre>1; cDNA; 1857 BI ransmembrane pro H INC. 100.00* 100.00*</pre>	cDNA; 1857 insmembrane INC.	100.00% : 100.00% 100.00%	DNA; 18 and tr	H INC. 100.00\$ : 100.00\$	i; cDNA; 1857 BP nan PRO polypept INC. 100.00\$ 100.00\$	1; CDNA; 1857 BP. nan PRO polypeptide #18 H INC. Conse 100.00\$ Misma		HINC. 100.00% 100.00% 100.00%	1; cDNA; 1857 BP cansmembrane PRO
PD 05-JUN-2003. PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	ID ADD09467 standard; cDNA; DE Human PRO polynucleotide PN 16-00194775-A1. PD 16-00T-2003. PA (GETH ) GENENTECH INC. PEICENT Similarity: 100.01 Best Local Similarity: 100.01 Query Match: 100.01	RESULT 173  ID ADD03923 standard; CDNA; 1857 BP.  DE Human secreted/transmembrane protein CDNA, PN US2003104381-A1.  PD 05-JUN-2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 100.00% Mismacch Query Match: 100.00% Indels:	KESULT 174 ID ADD01499 standard, DE Human secreted/tra PN US2003108983-A1. PD 12-UTN-2003. PA (GETH ) GENENTECH	Percent Similarity: Best Local Similarity: Query Match:	AESOLI 1/3 ID ADD41180 standard; c) DE Novel human secreted PN US2003201418-A1	PD 30-OCT-2003.  PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Ouery Match:	RESULT 176  RESULT 176  DE CDNA encoding human PRO polypeptide #10  PN US2003194769-A1.  PD 16-OCT-2003.  PA (GETH) GENENTECH INC.  Percent Similarity: 100.00% Mism  Dest Local Similarity: 100.00% Mism  Duery Match: 1011101.00% Mism  Duery Match: 1011101.00% Mism	9 standaro coding hur 94792-A1. 2003. GENENTECI larity:	Query Match: RESULT 178 ID ADD53611 standard; cDNA; DE Novel human secreted and	· 🖰 >-	DD 2017 DE Human secreted/transmembrane PRO polypeptide PN US2003105012-A1.

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Dest Local Similarity: 100.00$ mismatches: 0

Query Match: 100.00$ Indels: 0

RESULT 182

ID ADD02000 standard; CDNA; 1857 BP.

DE Human PRO polynucleotide #183.

PA US2003203430-A1.

PA GETH 9 GENEWITECH INC.

Percent Similarity: 100.00$ Mismatches: 0

Query Match: 100.00$ Mismatches: 0

Query Match: 100.00$ Mismatches: 0

RESULT 183

ID ADD54182 standard; CDNA; 1857 BP.

DE Novel human secreted and transmembrane protein PRO301 CDNA.

PA (GETH) GENEWIECH INC.

Percent Similarity: 100.00$ Mismatches: 0

Percent Similarity: 100.00$ Mismatches: 0

RESULT 184

RESULT 187

RESULT 187
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ADE32306 standard; cDNA; 1857 BP.
ADE32306 standard; cDNA; 1857 BP.
USOVE1 human secreted and transmembrane protein PRO301 cDNA.
USOVE194765-A1.
16-OCT-2003.
(GETH ) GENENTECH INC.
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US2003194779-A1.
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1D ADD92499 standard; CDNA; 1857 BP. DE Human PRO polynucleotide #183.

PN US2003199030-A1.

PA (CETH ) GENEWTECH INC.

Percent Similarity: 100.00% M Query Match: 1857 BP. 100.00% M Guery Match: 1857 BP. 100.00%

RESULT 185

ID ADD91395 standard; CDNA; 1857 BP. DE Human PRO polynucleotide #183.
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RESULT 181
ID AD02566 standard, cDNA, 1857 BP DE Human PRO polymucleotide #183.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GRNENTECH INC.
Percent Similarity: 100.00%
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DE04009 standard; cDNA; 1857 BP.
Human PRO polynuclectide #183.
US2003199057-Al.
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DE Human PRO Polynuclectide #183
D 23-OCT-2003.
PA (GETH) GENENTECH INC.
PACTECT Similarity: 100.00$
Best Local Similarity: 100.00$
RESULT 186
ID ADB04009 standard; cDNA; 1857
DE Human PRO POlynuclectide #183
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00$
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PA (GETH ) GENENTECH INC.
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PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%

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ID ADD51767 standard; c
DNA encoding human
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH IN
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20.00	dard ynuc Al.	G to m to	Human PRO polynuc US2003199025-A1. 23-OCT-2003.	PA (GETH ) GENENTECH INC. Percent Similarity: 100 Pest Local Similarity: 100 Query Match: 100 RESULT 198	ALDSTAIL BUGBLED, Human secreted/trail US2003077583-A1. 24-APR-2003. (GETH ) GENENTECH I	ity:	ID ADE18919 standard; cDb BE Human PRO polynucleoti PN US2003199026-A1. PD 23-0CT-2001	H L	1D ADEA115 Steandard; CDN BE Human PKO polymucleoti PN US2003199033-A1.	Percent Similarity: 100 Best Local Similarity: 100 Best Local Similarity: 100 RESULT 201 TD ADD95404 standard: CDN	DE Human PRO polynucleoti PN US2003199059-A1. PD 23-OCT-2003.	PA (GETH ) GENENTECH INC. Percent Similarity: 100 Best Local Similarity: 100 Query Match: 100 RESULT 202	DE CDNA encoding human PR US2003199064-A1.	PA (GETH ) GENENTECH INC. Percent Similarity: 100 Query Match: 100 REGULT 203	ID ADD/18908 strandard; CDN DE CDNA encoding human PR N US2003203429-A1. PD 30-0CT-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 100 Best Local Similarity: 100
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Percent Similarity: Best Local Similarity: Query Match:	KESULI 188  DE ADE22238 standard; CDNA; 1857 BP.  DE CDNA encoding human PRO polypeptide #183  PN US20031999056-A1.	(GETH ) GENENTECH Cent Similarity: tt Local Similarity: try Match:	ID ADD79462 standard; cDNA; 1857 BP. DE cDNA encoding human PRO polypeptide #183 US2003203428-Al.	30-OCT-2003. (GETH ) GENENTECH cent Similarity: it Local Similarity: rry Match:	ID ADB41998 standard; cDNA; DE Human PRO polynucleotide PN US2003194772-A1. PD 16-OCT-2003.	Percent Similarity: 1 Best Local Similarity: 1 Query Match: 1	KESULT 191  ID ADE17815 standard; CDNA;  DE Human PRO polynucleotide PN US2003199023-A1.	(GETH ) GENENTECH cent Similarity: t Local Similarity: ry Match:	KESULI 192 ID ADD91947 standard; CDNA; DE Human PRO polynucleotide PN US2003199053-A1.	GETH ) GENEWECH (GETH ) GENEWECH cent Similarity: st Local Similarity: sry Match:	ID ADE33410 standard; cDNA; 1857 BP DE Novel human secreted and transme PN US2003194767-A1.	PD 16-OCT-2003. PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	ID ADE33962 standard; cDNA; 1857 BP. DE Novel human secreted and transmembrane protein PN US2003194791-A1.	T-2003. ) GENENTECH milarity: Similarity: h:	RESULT 195  DD ADD80014 standard; cDNA; 1857 BP.  DE cDNA encoding human PRO polypeptide #183  PN 052003207417-A1.  PD 06-NOV-2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 100.00% Conser

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PRO polypeptide #183.
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PRO polypeptide #183.
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Match:	T 204 ADE32858 standard; cDNA; Novel human secreted and US2003194766-A1.	003. GENENTECH arity: milarity:	KESULT 205 ID ADE42550 standard; cDNA; 1857 DE Human PRO polynucleotide #183 PN US2003199032-A1. PD 23-OCT-2003.	SENENTECH arity: nilarity:	KESULI 206 ADDB0566 standard; CDNA; 1857 BP. DE CDNA encoding human PRO polypeptide #183 PN US200320/1418-Al.	PA (GETH) GENENTECH: Percent Similarity: Best Local Similarity: Query Match:	ADD89594 standard; cDNA; 1857 BP. Human PRO polynucleotide #183. 023003199028-A1.	PA (GETH) GENENTECH INC. Percent Similarity: 100.00% Best Local Similarity: 100.00% Query Match: 100.00%	12 208 BEEGOST Standard; CDNA; Human PRO polynucleotide US2003199031-A1.	PD 23-OCT-2003.  PD 23-OCT-2003.  Percent Similarity: Best Local Similarity: Query Match:	7 standard RO polynuc. 99034-Al. 2003. GENENTECH larity: imilarity:	6 standard; RO polynucl 84777-A1. 2003. GENENTECH larity: imilarity:	ADG21515 standard; cDNA; Novel human secreted and US2003207355-A1.	PA (GETH) GENENTECH : Percent Similarity: Best Local Similarity: Query Match:
Ouery	15	PD PA Perce Best Query	RESOL 1D DE PN	PA Perce Best Query	ID DE PN	PA Perce Best Query	PNE	PA Perce Best Query	ID ID PN	PD PA Perce Best Query	AESOLI ID DE PN PD PETCE Best Query	RESUL ID DE DN PN PA Perce Best Query	DE D	PA Perce Best Query

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1023156 standard, cDNA, 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
182003207384-Al.
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H155295 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
152003207381-A1.
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IS2003039972-A1.
                                                                                                                           scandard; cDNA; 1857 BP.
Human PRO polynucleotide #183.
6-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                    DG80003 standard; cDNA; 1857 BP.
uman PRO polynucleotide #183.
iS2003207372-A1.
                                                                                                                                                                                                                                                           DG80555 standard; cDNA; 1857 BP.
uman PRO polynucleotide #183.
iS2003207373-A1.
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DG63771 standard; cDNA; 1857 BP.
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DF97491 standard;
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cDNA encoding human PRO polypeptide #21
                JS2002192659-A1.
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                                                                                                                                             ADI64066 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207385-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADIG3514 standard; cDNA; 1857 BP.
Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207387-Al.
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US2003207377-A1.
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Novel human secreted and transmembrane protein PRO301 CDNA.
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US2003207386-A1.
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ADI38013 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA, #25.
US2003054352-A1.
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US2002146709-A1.
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ACA58390 standard; cDNA; 1857 BP.
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                                 US2003-0-2003.
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(GETH ) GENENTECH INC.
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ID ADI38013 standard; cb Human secreted/trans
PN US200305435-A1.
PD 20-MAR-2003.
PA (GERH) GENENTECH IN
Percent Similarity: 1
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PD 13-FEB-2003.
PA (GETH) GENENTECH II
Percent Similarity:
Best Local Similarity:
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ACD42376 standard, cDNA, 1857 BP.

Novel human secreted and transmembrane protein PRO301 cDNA.
US2003040014-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003087355-A1.
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Novel human secreted and transmembrane protein PRO301 cDNA.
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US2003087356-A1.
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Novel human secreted and transmembrane protein
US2003087353-A1.
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PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
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PA (GETH) GENENTECH INC.

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RESULT 236
ID ADN14840 standard;
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ID ADN16573 standard;
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RESULT 233
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Conservative: Mismatches: Indels:	1857 BP. transmembrane protein PI	Conservative: Mismatches: Indels:	7 BP. protein cDNA, #25.	Conservative: Mismatches: Indels:		Conservative: Mismatches: Indels:		Conservative: Mismatches: Indels:		Conservative: Mismatches: Indels:	in cDNA, #25.	Conservative: Mismatches: Indels:		Conservative: Mismatches: Indels:	
0000	DNA; and	INC. 100.00\$ 100.00\$ 100.00\$			cDNA; 1857 BP. eotide #183.	INC. 100.00% 100.00% 100.00%	cDNA; 1857 BP. sotide #183.	* * *	; cDNA; 1857 BP. leotide #183.		CDNA; 1857 BP. 1smembrane prote	1 INC. 100.00% 100.00% 100.00%	cDNA; 1857 BP.		CDNA; 1857 BP.
PA (GETH) GENENTECH I Percent Similarity: Best Local Similarity: Query Match: RESULT 237	ID ADC81102 standard; c DE Novel human secreted PN US2003092115-A1.	PD 15-MAY-2003.  PA (GETH) GENENTECH I Percent Similarity: Best Local Similarity: Guery Match:	ID ADE79196 standard; CDNA; 185: DE Human secreted/transmembrane BN US2003135025-A1.	PA (GETH ) GENENTECH INC. Percent Similarity: 100.00% Best Local Similarity: 100.00% Query March: 100.00%	DE Human PRO polynucleotide PN US2003100087-A1.	PA 25-FM1-2003. PA (GETH) GENENTECH I Percent Similarity: Best Local Similarity: Query Match:	KESULI 240 ID ADD87914 standard; CDNA; DE Human PRO polynucleotide PN US2003022113-A1.	PD 15-MAY-2003. PA (GETH) GENENTECH I Percent Similarity: Best Local Similarity: Query Match:	8 standard, RO polynuc] 03440-A1.	30-OCT-2003. (GETH ) GENENTECH : cent Similarity: tt Local Similarity: xry Match:	DE ADE79620 standard; cDNA; 1857 BP. DE Human secreted/transmembrane protein cDNA, PN US2003130489-A1.	PD 10-JUL-2003. PA (GETH ) GENENTECH I PETCENT SIMILATILY: Best Local Similarity: Ouery March:	ADE75766 standard, Human PRO polynucl US2003211571-A1.	PD 13-NOV-2003.  PAA (GETH) GENERICH INC.  PROCENT SIMILARITY: 100.00%  Best Local Similarity: 100.00%  Query Match: 100.00%	RESULT 244 ID ADE73296 standard; cDNA; 1857 BP.

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cDNA encoding human PRO polypeptide #183.

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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207360-A1.
06-NOV-2003.
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003201426-A1.
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CDNA encoding human PRO polypeptide #183.
US2003207376-A1.

06-NOV-2003.

(GETH ) GENENTECH INC.

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ID ADG02281 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% MESUL Cocal Similarity: 100.00% IRESULT 269
ID ADG22067 standard; cDNA; 1857 BP.
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US2003208055-A1.
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Human PRO polynucleotide #183.
US2003207422-Al.
06-NOV-2003.
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ADG16751 standard; cDNA; 1857 BP.
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PN US20030736-A1.
PD 66-NOV-2003.
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DB CDNA encoding human
PN US2003207376-A1.
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CDNA encoding human PRO polypeptide #183.
US2003207425-A1.
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cDNA encoding human PRO polypeptide #183.
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cDNA encoding human PRO polypeptide #183.
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3207374-A1. V-2003. ) GENENTECH milarity: Similarity: h:	ADG23708 standard; cDNA; novel human secreted and	NOV-2003. STH ) GENENTECH Similarity: al Similarity: ttch:	standard; O polynucl 7423-A1. 003. GENENTECH arity: milarity:	RESULT 287  ID ADG24898 standard; cDNA; DE Novel human secreted and PN 11S20013207427-A1	003. GENENTECH arity: milarity:	ADG07195 standard; cDNA; Novel human secreted and US2003207350-A1.	PD 06-NOV-2003.  PERCENT (GETH) GENENTECH PERCENT Similarity: Best Local Similarity: Query Match: RESHIT 289	7 standard; uman secret 07356-A1.	FD 08-NOV-2003. PA (GETH) GENETECH Percent Similarity: Best Local Similarity: Query Match:	NDG55242 standard; cDNA; NOVel human secreted and US2003194778-Al.	T-2003. ) GENENTECH milarity: Similarity: h:	906 standard; human secret 3207390-A1.	PD 06-NOV-2003.  Per (GETH ) GENENTECH : Percent Similarity: Best Local Similarity: Ouery Match:	ADG62010 standard; cDNA; 1857 BP Novel human secreted and transmer US2003207428-A1.
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PN 06-NOV-2003.
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PA (GETH) GENEWIECH INC.
Percent Similarity: 100.00$ Conservative: 0
Best Local Similarity: 100.00$ Mismatches: 0
Query Match: 100.00$ Indels: 0
RESULT 295
ID ADG57450 standard; cDNA; 1857 BP.
DE Novel Human secreted and transmembrane protein PRO301 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENEWIECH INC.
Percent Similarity: 100.00$ Mismatches: 0
CONSERVATIVE: 0
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3SULT 296
1 ADG56898 standard; cDNA; 1857 BP.
E Novel human secreted and transmembrane protein PRO301 cDNA.
N US2003207364-A1.
D 06-NOV-2003.
A (GETH ) GENENTECH INC.
ercent Similarity: 100.00$ Mismatches: 0
lest Local Similarity: 100.00$ Mismatches: 0
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US2003207420-A1.
06-NOV-2003.
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A (GETH) GENENTECH INC.

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Mismatches:
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N US2003027145-A1.

D 06-FRB-2003.

A (GFTH) GENENTECH INC.

Percent Similarity: 100.00% Mismatches:
Nest Local Similarity: 100.00% Indels:
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D ADGB2211 standard; CDNA; 1857 BP.
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Human secreted/transmembrane protein cDNA, #25:
US2003027146-A1.
06-FEB-2003.
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D ADG92214 standard; cDNA; 1857 BP
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US2003207358-A1.
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A (GETH) GENENTECH INC.

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t Local rry Matci ULT 309	DE NOVEL NUM PN US2003207 PD 06-NOV-20 PA (GETH ) G	일 후 맞닭	DE Human PRO PN US2003194 PD 16-OCT-20 PA (GETH ) G	97 7 2	DE Novel hum PN US2003207 PD 06-NOV-20 PA (GRTH ) G	it it	DE NOVEL NUM PN US2003207 PD 06-NOV-20 PA (GETH ) G	Percent Simila Best Local Sim Query Match: RESULT 313	1D ADG51458 DE Novel hum PN US2003207 PD 06-NOV-20	PA (GETH ) G Percent Simila Best Local Sim Query Match: RESULT 314		PA (GETH ) G Percent Simila Pert Simila Best Local Sim Query Match: RESULT 315	1D ADG54690 DE Novel hum PN US2003207 PD 06-NOV-20	gr tr ce	1D ADG59730 DE Novel hum PN US2003207 PD 06-NOV-20 PA (GETH ) G	rce st ]
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PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	KESULI 301  ID ADG58002 standard; cDNA; 1  DE Novel human secreted and t  PN US2003207363-A1.	PD 06-NOV-2003. PA (GETH) GENENTECH INC. Percent Similarity: 100.00% Best Local Similarity: 100.00% Query Match:	RESULT 302 ID ADG53586 standard; cDNA; DE Novel human secreted and PN US2003207415-A1.	PD 06-NOV-2003. PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	RESULT 303 ID ADG71472 standard; cDNA; DE Novel human secreted and PN IS2003207421-A1.	ពួកម្	RESUL! 304 DD ADG81659 standard; cDNA; DE Human PRO polynucleotide PN US2003207805-A1.	از تر ن	RESOLI 305 ID ADH30621 standard; cDNA; DE Human PRO polynucleotide PN US2003077723-A1.	24-APR-2003. (GETH ) GENENTECH :Cent Similarity: it Local Similarity: iry Match:	DE ADG63620 standard; cDNA; 1857 DE Human secreted/transmembrane PN US2003180796-A1.	in in in	KESULI 307 ID ADH11988 standard; CDNA; DE Novel human secreted and PN US2003207419-A1.	13 th 12	KESULT 30B ID ADG52410 standard; cDNA; DE Novel human secreted and PN US2003207414-A1. PD 06-NOV-2003.	PA (GETH ) GENENTECH INC Percent Similarity: 10

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Query Match: RESULT 317	ID ADH20430 standard; cDNA; 1857 BP. DE Human secreted/fransmembrane procein PN US2004005553-A1. PD 08-JAN-2004. PA (GFTH) GENENTECH INC. Percent Similarity: 100.00\$ Best Local Similarity: 100.00\$	Query Macch: RESULT 318 ID ADH43486 standard; DE Human PRO polynucle: N US2003224984-A1. PD 04-DEC-2003. PA (GETH ) GENENTECH II PErcent Similarity: Best Local Similarity: Query Match:	S standard 6creted/tr 06211-A1. 2004. 2000-KS GODDARD A GODDARD A GUNNEY A MATHER J WOOD W I.	TESOUL 3.26  ID ADHS9830 standard; cDNA; 185;  DE Human secreted/transmembrane  N US200315904-A1.  PD 20-NOV-2003.  PA (GETH ) GENENTECH INC.  PA (GETH) GENENTECH INC.  Best Local Similarity: 100.00\$  OUMERY MATCH: 100.00\$	RESULT 3.41  DE Human secreted/transmembrane protein CDI BN US2004005665-A1. PN US.2004005665-A1. PA (GDD)/ GDDBARD A. PA (GDD)/ GDDBARD A. PA (GDD)/ GDDBARD A. PA (GUN) GROWSKI P J. PA (GUN)/ GROWSKI P J. PA (GUN)/ GUNSKI P J. PA (WILL)/ MATHER J P. PA (WILL)/ WILLIAMS P M.	milarity: milarity: standard; oding huma 7361-A1.	(GETH ) GENENTECH cent Similarity: str Local Similarity: sty Match: sULT 323 AD118600 standard; Human secreted/tra US2003152999-A1. 14-AUG-2003. (GETH ) GENENTECH

Dercent Similarity: 100.00% Mismacches: 0  Best Local Similarity: 100.00% Mismacches: 0  RESULT 324  RESULT 324  RESULT 324  RESULT 325  B Human secreted/transmembrane protein CDNA, #25.  PD 07-AUG-2001.  Percent Similarity: 100.00% Mismacches: 0  GUSTY Match: 100.00% Mismacches: 0  GUSTY Match: 100.00% Mismacches: 0  DE Human secreted/transmembrane protein CDNA, #25.  DE AUGUSTO 30906340-A1.  PA (GETH) GENEWINER INC.  DE COMBERTICH: 100.00% Mismacches: 0  RESULT 326  IN US2000059540-A1.  DE NOVOR Human secreted and transmembrane protein PR0301  PR 10570190500-A1.  DE NOVOR Human secreted and transmembrane protein PR0301  PR 10570190500-A1.  DE NOVOR Human secreted and transmembrane protein PR0301  DE NOVOR HUMAN SECRETED SIMI		cdna.	CDNA.	CDNA.
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	Percent Similarity: Best Local Similarity: Query Match: RESULT 324 ID AD165320 standard; DE Human Secreted/tra PN US2003148419-A1. PD 07-AUG-2003. PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Cuery Match: RESULT 325 ID AD137583 standard; DE Human secreted/tra PN US2003096340-A1.	PD 22-MAY-2003.  PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Query Match: RESULT 326  ID MOVEL human secret PN US2004009548-A1. PD 15-JAN-2004. PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Query Match: RESULT 327  ID ADH97379 standard; DE Human secreted/transparent and	PN US2003190610-A1. PD 09-OCT-2003. PA (GETH) GENERTECH Percent Similarity: Guery Match: RESULT 328 ID AD115368 standard; DE NOVel human secret PN US2003207382-A1. PD 06-NOV-2003. PA (GETH) GENENTECH Percent Similarity: Query Match: RESULT 329 ID ADG9245 standard; DE NOVEL Numan secret Percent Similarity: Query Match: RESULT 329 ID ADG9245 standard; PN HS20044009547-A1.	PD 15-JAN-2004. PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Query Match: RESULT 330 ID AD165747 standard; DE Human secreted/trapp UNACON CONTROL OF AUGUSTON CONTROL OF

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RESULT 344
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Novel human secreted and transmembrane protein PRO301 cDNA.
US2003207349-A1.
06-NOV-2003.
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US2003186358-A1.
02-OCT-2003.
                                                                            ADH60490 standard; cDNA; 1857 BP.
Human secreted/transmembrane protein cDNA, #25.
US2004023331-A1.
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US2003096233-A1.
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US2003190611-A1.
     Mismatches:
Indels:
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PN US2C031c.

PN GETH ) GENENTEC.

PA (GETH ) GENENTEC.

Percent Similarity:

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ADM25081 standard; cDNA; 1857 BP.

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PA 02-CT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00$
Best Local Similarity: 100.00$
REGULT 335
ID ADL08740 standard; cDNa; 1857 BP.
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RESULT 334
ID ADJ9547 standard; cDNA; 1857 BP.
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RESULT 338
ID 338
BESULT 338
BESULT 338
DE Human secreted/transmembrane prot
PD 09-007-2003.
PD 09-007-2003.
PA (GETH ) GENENTECH INC.
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Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
RESULT 339
ID AD.77.7.7.
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PA (GETH ) GENENTECH INC.

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
                                                                         D ADMO190 standard; cDNA, DE Human secreted/transmemth US200402331-A1.

PA US200402331-A1.

PA (GDDA) GDDARD A.

PA (GDDA) GODOWSKB I.

PA (GDDA) GODOWSKB A.

PA (GURN) GURNEY A I.

PA (WILL) MATHER J P.

PA (WILL) MATHER J P.

PA (WILL) WILLIAMS P M.

PA (WILL) WILLIAMS P M.

PA (WOOD) WOOD W I.

PECCENT SIMILATICY: 100.

QUELY MATCH:
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Best Local Similarity:
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RESULT 332
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RESULT 343
ID ADM42453 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2004058424-Al.
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cDNA encoding human PRO polypeptide #183.
US2004038335-A1.
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US2004077064-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID AD006153 standard; CDNA; 1857 BP.
DE Human PRO polynucleotide #23.
DV US6686451-B1.
DD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Metch:
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RESULT 346
TD ADR17914 standard; CDNA; 1857 BP.
                                                                                                           CDNA; 1857 BP
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Human PRO polynucleotide #183
US2004038336-A1.
                                                                                                                         Human PRO polynucleotide #27
US2004043927-A1.
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PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
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PD 04-MAR-2004.
PD (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
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PA (GETH ) GENENTECH INC.
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Best Local Similarity: 100.00$
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                                    PA (GETH) CONTROL INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
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Percent Similarity: 100.00%
Best Local Similarity: 100.00%
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PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match:
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DESNOYERS L.
EATON D L.
FERRARA N.
FILVAROFF E.
FONG S.
                                                                           Query Match...
RESULT 340
Th ADK82831 standard; C
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(BOTS/) BOTSTEIN D.
(DESN/) DESNOYERS L.
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ID ADM27729 standard;
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29-JUL-2004.
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                          26-FEB-2004.
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(FERR/)
(FILV/)
(FONG/)
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GRIMALDI C J.

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AD195349 standard; CDNA; 1857 BP.

Movel human secreted and transmembrane protein PRO301 CDNA.
US200320734-A1.

06-NOV-2003.
(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
Local Similarity: 100.00$ Conservative: 0
Local Similarity: 100.00$ Mismatches: 0
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US2003152922-A1.
14-AUG-2003.
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Indels:
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CDNA encoding human PRO polypeptide #183.
US2003077659-A1.
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US2004185531-A1.
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RESULT 349
Th ADT03590 standard; cDNA; 1857 BP.
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ADS74553 standard; CDNA; 1857 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA; 1857 BP.
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Human PRO301 cDNA sequence.
AU2003259607-A1.
27-NOV-2003.
(GETH) GENENTECH INC.
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Local Similarity: 100.00%
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PAONI N F.
ROY M A.
STEWART T A.
TUMAS D.
WILLIAMS P M.
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GODDARD A.
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DESNOYERS L.
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                                                                                        GURNEY A L.
HILLAN K J.
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GODDARD A
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                             GODOWSKI
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(BOTS/)
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FONG/)
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Human secreted protein-encoding gene 23 cDNA clone HACAA29, SEQ ID NO:33.
WO200136440-A1.
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WO200136440-A1.
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Novel coding sequence (useful for identifying genetic disorders) #193.
WO2003054152-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADR46572 standard; DNA; 2009 BP.
Human JAM-1, FI1 receptor (F11R) transcript variant 4, encoding gene.
JP2004242513-A.
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Novel DNA-related contig nucleotide seguence #139.
WO2003054152-A2.
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Mismatches:
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Human cDNA encoding a novel human protein #275.
WO200155437-A2.
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WO200155437-A2.
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PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 100.00$
Best Local Similarity: 100.00$
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PA (HUMA-) HUMAN GENOME SCI INC.
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PAONI N F.
ROY M A.
STEWART T A.
TUMAS D.
WILLIAMS P M.
GURNEY A L.
HILLAN K J.
KLJAVIN I J.
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RESULT 356
Th AAD08335 standard; cf
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PA (HYSE-) HYSEQ INC.
Percent Similarity: 1
Best Local Similarity: 1
Query Match: 1
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Best Local Similarity:
Query Match:
RESULT 352
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Percent Similarity:
Best Local Similarity:
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Percent Similarity:
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Percent Similarity:
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                                                                                                                                 (WITT/)
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Percent Best Loc Query Ms RESULT 3 RESULT 3 RESULT 3 RESULT 3 RESULT 3	DE PN PD PD PA	Percent Best Loo Ouery Me RESULT	1D ADS		ID ADA DE HUI PN JPS	PA (DE PACCENT PACENT PERCENT PACENT	Query Ma RESULT 3	OI DE COMPANY		Best Loc Query Ma RESULT 3	ID DE		Percent Best Loc Query Me	TEGULI 1	Percent Percent Best Loc Query Ma	A CONTRACTOR OF THE CONTRACTOR	PA (GF Percent Best Loc Query Mc REGULT 31	OT O
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KAGAKU GIJUTSU SH Conservative: Mismatches: Indels:	):53.	Conservative: Mismatches: Indels:	. 3364.	Conservative: Mismatches: Indels:	3364.	Conservative	Mismatches: Indels:	nan clone cDNA,		Conservative: Mismatches: Indels:			Conservative: Mismatches:	inaeis: protein #39.	Conservative: Mismatches: Indels:	CDNA 28094.	CCINE INC. Conservative: Mismatches: Indels:	CDNA 22257.
YOSEI HOJIN 100.00% 100.00% 100.00%	CDNA; 2100 BP. 3 CDNA SEQ ID NO:	MEDICAL RES. 100.00% 100.00%	CDNA; 2141 BP. CDNA, SEQ ID NO:	NST. 100.00\$ 100.00\$	; cDNA; 2141 BP. cDNA clone SegID	BIOTECHNOLOGY.	100.00%	cDNA; 2141 BP. preparation human		100.00% 100.00% 100.00%	.87 BP.		INC. 100.00% 100.00%	100.00* cDNA; 2259 BP. ; a novel human	100.00% 100.00% 100.00%	ırd; cDNA; 3389 BP. expression marker o	PREDICTIVE MEDICINE INC 100.00% Conserva 100.00% Mismatch 100.00% Indels:	
PA (DOKU-) DOKURITSU G Percent Similarity: Best Local Similarity: Query Match: RESULT 359	ID ADL26799 standard; cDE Human JAM1 encoding PN WO2004022778-A1. PD 18-MAR-2004.	(GARV-) GARVAN INST ent Similarity: Local Similarity: //Match:	RESULT 360 ID AAK94509 standard; DE Human full-length c	05-SEF-2001. (HELL ) HELLX RES I she Similarity: Local Similarity: , Match:	KESOLI 361 ID ADL31331 standard; DE Full length human c	10-MAR-2004. (REAS-) RES ASSOC B	Similarity: h:		_	ilarity: Similarity: 1:		028479-A2.	GENENTECH arity:	ndard; ncoding A2.	UUI. HYSBQ INC. arity: milarity:	anda ate -A2.	001. MILLENNIUM arity: milarity:	standard;

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NR46576 standard; DNA; 3861 BP.
nman F11 receptor (F11R) transcript variant 4, encoding gene, SEQ ID 7.
P2004242513-A.
                                                                                                  RA6570 standard; DNA; 3660 BP.
uman JAM-1, F11 receptor (F11R) transcript variant 1, encoding gene.
P2004242513-A.
                                                                                                                                                                                                                                                                                                               5, encoding gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ61781 standard; cDNA; 1421 BP.
NNA encoding human A33 receptor homologue, SEQ ID NO:254.
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DNA encoding human A33 receptor homologue, SEQ ID.NO:70.
99955865-A1.
                                                                                                                                                                                                                                                                                      RA6578 standard; DNA; 3794 BP.
nman JAM-1, F11 receptor (F11R) transcript variant
P2004242513-A.
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uman cDNA isolated from skin cells SEQ ID NO: 254.
0200190357-A1.
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DOKUT: DOKURITSU GYOSBI HOJIN KAGAKU GLJUTSU SH.

L Similarity: 100.00% Conservative:
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natch:
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DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
t Similarity: 100.00$ Conservative:
ocal Similarity: 100.00$ Mismatches:
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DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
L Similarity: 100.00% Conservative:
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GENE-) GENESIS RES & DEV CORP LTD.
It Similarity: 99.33% Conservative:
MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
t Similarity: 100.00% Conservative:
ocal Similarity: 100.00% Mismatches:
Macch: 100.00% Indels:
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It Similarity: 99.67% Cc

cocal Similarity: 99.67% Mi
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GENE-) GENESIS RES & DEV CORP LTD.

CC Similarity: 99.67% Misonal Similarity: 99.67% Misonal Similarity: 99.48% Ir
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GENE.) GENESIS RES & DEV CORP LTD.
IC Imilarity: 99.67% C.
Iccal Similarity: 99.67% M
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Skin cell cDNA, SEQ ID NO: 70.
23-NOV-2000.
(GENE-) GENESIS RES & DEV CORP LTD.
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kin cell cDNA, SEQ ID NO: 254.
2200069884-A2.
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Conservative: Mismatches: Indels:	BP. cells SEQ ID NO: 7	LID. Conservative: Mismatches: Indels:	66 BP. consensus sequence.	Conservative: Mismatches: Indels:	) BP. SEQ ID NO:119.	Conservative: Mismatches: Indels:	seg id NO:118.	Conservative: Mismatches: Indels:	o mRNA; 924 BP. molecule gene.	AG F. Conservative: Mismatches: Indels:	BP. cDNA SEQ ID No 30.	Conservative: Mismatches: Indels:	BP.  Conservative: Mismatches:	Indels: BP. 120.
99.33% 99.33% 99.22%	cDNA; 1421 d from skin	S & DEV CORP 99.33\$ 99.33\$	0	INC. 99.34% 99.00% 98.12%	, 4249 gene	INC. 84.66% : 84.66% 96.31%	, 4633 gene	INC. 62.29% 62.29% 92.36%	d; cDNA to mRNA adhesion molec	A ROCHE & CO 94.65% 93.65% 91.16%	cDNA; 1812 in encoding	ME SCI INC. 91.97% 91.97% 90.45%	CDNA; 1812 NO: 120. ME SCI INC. 91.97% 91.97%	90.45% cDNA; 1812 B de SEQ ID NO
Percent Similarity: Best Local Similarity: Query Match:	RESULT 375 ID ABL34760 standard; OB Human CDNA isolated PN WO200190357-A1.	PD 29-NOV-2001. PA (GENE) GENESIS RES Percent Similarity: Best Local Similarity: Ouery Match:	DAX37716 standard; DNA; 2 DE Aux37716 standard; DNA; 2 DE Human cDNA clone DNA35936 DN WO9914241-A2	-MAR-1999. ETH ) GENENTECH Similarity: cal Similarity:	SULI 3// ADJ67405 standar Human ovarian sp WO2004013311-A2.	1004. DIADEXUS arity: milarity	ACSOLIA 3/0 ID ADJ67404 scandard; DNA, DE Human ovarian specific PN W02004013311-A2. PD 12-FFR-2004	PA (DIAD-) DIADEXUS II Percent Similarity: Best Local Similarity: Guery Match:	andar ional 1.	PD 11-JUN-1998.  PA (HOFF) HOFFMANN LA PErcent Similarity: Best Local Similarity: Query Match:	AAS28784 standard; Human immunoglobul WO200155315-A2.	PD 02-AUG-2001. PD (10-AUG-2001. PDA (HUMA-) HUMAN GENOME PErcent Similarity: 9 Best Local Similarity: 9 Guery Match: 9 PERCENT 2011	ID ABA06454 standard; cl DE Human CDNA SEQ ID NO PN WC200154474-A2. PD 02-AUG-2001. PA (HUMA) HUMAN GENOME Percent Similarity: 9; Best Local Similarity: 9;	Weery Match: RESULT 382  ID ABV83791 standard; CDN DE Human polynucleotide 5 PN US2002090672-A1. PD 11-UTL-2002. PA (ROSE/) ROSEN C A. PA (RUBE/) RUBEN S M.

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DE Human JAM-1, F11 receptor (F11R) transcript variant 3, encoding gene.
DE Human JAM-1, F11 receptor (F11R) transcript variant 3, encoding gene.
DE Human JAM-1, F11 receptor (F11R) transcript variant 3, encoding gene.
DE JORGA 242513-A.
PD 02-SEP-2004
DA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Percent Similarity: 86.29$
Mismatches: 1
Query Match: 83.35$
Indels: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAK93330 standard; cDNA; 790 BP.
Human cDNA clone representative sequence, SEQ ID NO: 1790.
Bli30094-A2.
05-SEP-201.
(HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADL29757 standard; CDNA; 790 BP.
5' end of a representative human cDNA cluster SeqID 1790.
EP1396543-A2.
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Human CD-like molecule HKACI03 cDNA, SEQ ID NO:145.
WO200226930-A2.
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                                                                                  ADB31509 standard; cDNA; 1812 BP.
Human cDNA encoding a novel protein SEQ ID NO
US2003077606-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DE Human cDNA encoding a novel human protein #40.
DE Human cDNA encoding a novel human protein #40.
DE Human cDNA encoding a novel human protein #40.
PA WC200155437-A2.
PA (HYSE-) HYSEQ INC.
PA (HYSE-) HYSEQ INC.
Beccent Similarity: 85.95% Mismatches:
Ouery Match: Indels:
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Indels:
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DE T cell activation associated cDNA #35.

PN WG2004058805-A2.

PD 15-UUL-2004.

PA (ASAH-) ASAHI KASEI PHARMA CORP.

Percent Similarity: 86.29% Mismatc Query Match:

RESULT 386.
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Lul 10-MRR-2004.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

Percent Similarity: 97.10%

Dest Local Similarity: 97.10%

Query Match: 78.50%

ID AAX21838 standard; rr.

DE F11 antigen Cod':

PD 21-78".
                                                                           ID ADES.—
DE Human CDNA e...

PN US200307666-A1.

PD 24-PR-2003

PA (HUMA-) HUMAN GENOME SCI INC.

Percent Similarity: 91.97%

Best Local Similarity: 91.97%

"atch:
                                                                                                                                                                                                                                     ID ADR41346 standard; cDNA; 1897 B
DE Human CD-like molecule HKACIO3
PN W0200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 91.97%
Query March:
RESULT 385
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PD 05-SEP-2001.
PA (HELL) HELLX RES INST.
Percent Similarity: 97.10%
Best Local Similarity: 97.10%
                 91.97%
91.97%
90.45%
PA (BARA/) BARASH S C.
Percent Similarity; 91
Bueft Local Similarity; 91
Query Match:
RESULT 383
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RESULT 388
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ADN35287 standard; DNA; 726 BP.
Human PRO301 DNA fragment consens01.
WO2004031105-A2.
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                                                                                                                                                                                              PN W09927098-AZ.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 99.07%
Best Local Similarity: 98.60%
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PD 15-APR-2004.
PD 15-APR-2004.
Percent Similarity: 99.07%
Best Local Similarity: 98.60%
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PA (GEMY ) GENETICS INST INC. Percent Similarity: 99.49$ Best Local Similarity: 99.49$
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC
Percent Similarity: 82.'
Best Local Similarity: 71.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GURN/) GURNEY A L.
(NAPI/) NAPIER M A.
(TUMA/) TUMAS D.
(WOOD/) WOOD W I.
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GODDARD A.
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Best Local Similarity:
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WO9845437-A2.
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(GODD/) (GURN/) (
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RESULT 396
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RESULT 398
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RESULT 402
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RESULT 397
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RESULT 399
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Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4051.
WO2003065993-A2.
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Human polynucleotide SEQ ID NO 94.
US2002090672-Al.
                                                                                                 ABA06428 standard; cDNA; 1894 BP.
Human cDNA SEQ ID NO: 94.
WO200154474-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACA10115 standard; cDNA; 750 BP. Human NOVX polynucleotide #5. WO200290504-A2.
                                                                                            ID ABL.

DE Human CDNA C.

PN WO2001544-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Percent Similarity: 85.71%

Best Local Similarity: 75.75%

Onery Match: 72.73%
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DE Human NOVX polynucleotide #5.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 75.25#
Best Local Similarity: 75.25#
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Human NOVX polynucleotide #5.
US2004018594-Al.
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                                                                                                                                                                                                                                                                                                                       ID ABV83765 standard; cDNA; 1865
DE Human polynuclectide SEQ ID
DV US2002096672-A1.
PD 11-JUL-2002.
PA (ROSE)/ ROSEN C A.
PA (RUBE)/ RUBEN S M.
PA (RARA/) BARASH S C.
Percent Similarity:
Best Local Similarity:
RESULT 393
  91.25%
90.87%
74.68%
Percent Similarity:
Best Local Similarity:
Query Match:
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ADH62531 standard; DNA; 726 BP.
Human consen01 DNA used to isolate DNA40628 encoding PRO301 protein.
US2003171568-A1.
11-SEP-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADR46580 standard; DNA; 2453 BP.
Mouse junctional adhesion molecule-1 encoding gene, SEQ ID 11.
JP200424513-A.
O2-SEP-2004.
                                                                                                                                                                                                                       ABX93346 standard; cDNA; 726 BP.
Consensus sequence expressed sequence tag, EST, consen01.
US200218206-A1.
05-DEC-2002.
(GETH ) GENENTECH INC.
(GETH ) 99.07$
Conservative: 1
Local Similarity: 98.60$
Mismatches: 0
Match:
33
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Percent Similarity: 83.06$ Conservative:
Best Local Similarity: 68.44$ Mismatches:
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Mismatches:
Indels:
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Mismatches:
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Mismatches:
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Mismatches:
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PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

Percent Similarity: 82.72* Conservative: Best Local Similarity: 68.11* Mismatches:
Conservative:
                Mismatches:
                                                                AAX81767 standard, DNA, 726 BP.
Nucleotide sequence used to isolate DNA40628.
WO9927098-A2.
                                  Indels:
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WO2004031105-A2.
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RESULT 415
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Human DNA35936 used to isolate DNA40628 encoding
US2003171568-A1.
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Mismatches:
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Consensus assembly expressed sequence tag, EST,
US2002182206-A1.
05-DEC-2002.
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Mismatches:
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Mismatches:
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                          ADK40843 standard; cDNA; 721 BP.
DNA encoding human platelet F11 receptor #2
US6699688-B1.
                                                                                                                                                             AAK92200 standard; cDNA; 605 BP.
Human cDNA 5'-end sequence, SEQ ID NO: 660.
EP1130094-A2.
                                                                                                                                                                                                                                                                                            5' end of a human cDNA molecule SeqID 660.
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                                                       PN US669968-B1.
PD 02-MAR-2004.
PA (UYNY) UNIV NEW YORK STATE RES FOUND.
Percent Similarity: 98.32% Cons
Best Local Similarity: 97.21% Mism
Query Match: 58.94% Inde
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Human PRO301 DNA fragment DNA35936.
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PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 93.14%
Best Local Similarity: 92.57%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX37715 standard; DNA; 390 BP.
Human cDNA clone DNA35936.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX81766 standard; DNA; 390 BP
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DA 25-MAR-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
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PA (GETH ) GENENTECH INC.

Percent Similarity: 100.00%

Best Local Similarity: 43.98%

Query Match:
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92.57%
51.13%
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It Similarity: 93.14%

Local Similarity: 92.57%

Match: 51.13%
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GODDARD A.
                                                                                                                                                                                                                                                                                      r 405
ADL28627 standard;
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PA (WOOD/) WOOD W I.
Percent Similarity:
Best Local Similarity:
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(GODD/) C
(GURN/) C
(NAPI/) N
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RESULT 405
Query Match:
RESULT 403
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PD 05-8
PA (HE1
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AAZG1659 standard; cDNA; 403 BP.
cDNA encoding human skin cell transmembrane protein, SEQ ID NO:54.
WO9955865-A1.
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WO200155320-A2.
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DNA encoding human prostate cancer antigen, Seq ID No
WO200155316-A2.
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Mismatches:
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Human cDNa isolated from skin cells SEQ ID NO:
WO200190357-A1.
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Percent Similarity: 100.00$

Best Local Similarity: 100.00$

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Percent Similarity: 100.00%
CBest Local Similarity: 100.00%
Query Match: 37.31%
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                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC99592 standard; cDNA; 403 BP. Skin cell cDNA, SEQ ID NO: 54. WO200069884-A2.
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Human cDNA SEQ ID NO: 116.
W0200154474-A2.
CJ-VGG-2001.
(HUMA-) HUMAN GENOME SCI INC.
cent'Similarity: 98.21%
                                                                                                           DNA; 415 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
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(HUMA-) HUMAN GENOME SCI INC.
sent Similarity: 98.21*
Local Similarity: 97.32*
y Match: 35.62*
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                                                                                                                            Human AA101561 DNA fragment WO9914241-A2.
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Local Similarity: 100.00%
                                 Percent Similarity: 100.00%
Best Local Similarity: 100.00%
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97.32%
35.62%
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Best Local Similarity: 97.54%
Query Match: 38.67%
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Best Local Similarity: 97.32%
Query Match: 35.62%
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                                                                                                                                                              25-MAR-1999.
(GETH ) GENENTECH INC.
15-APR-2004.
(GETH ) GENENTECH INC.
                                                                                                           AAX56510 standard;
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PD 02-AUG-2001.  PA (HUMA-) HUMAN GENOME Percent Similarity: 94 Best Local Similarity: 97 Query Match: 35	ME SCI INC. 98.21% 97.32% 35.62%	Conservative: Mismatches: Indels:	181
KESULI 419 ID ABV83787 standard; cDN DE Human polynucleotide S PN US202090672-A1.	CDNA; 425 BP. de SEQ ID NO 116	. 9	
PA (ROSE/) ROSEN C A. (ROSE/) ROSEN C A. PA (RUBE/) RUBEN S M. PA (BARA/) BARASH S C.			
ccent Similarity:	98.218	Conservative: Mismatches:	2 2 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
Query Macch: RESULT 420 ID ADB31543 standard; CI DE Human CDNA encoding a	35.62% CDNA; 425 BP. g a novel protein	indeis: in SEQ ID NO 64	<b>-</b>
5	ME SCI INC.	Conservative	-
Best Local Similarity: Query Match:	97.32% 35.62%	Mismatches: Indels:	1221
RESULT 421  ID ADJ09125 standard; DNA; 425 BP. DB Human prostate cancer associated	DNA; 425 BP. cer associated	gene SeqID71.	
	CMT TOO GV		
Percent Similarity: Best Local Similarity:	98.218 97.328	Conservative: Mismatches:	1 2 2
Query Match: RESULT 422		Indels:	1
standaro 7045 DNA	1; DNA; 435 BP. fragment.		
PN WO9914241-A2. PD 25-MAR-1999.			
GENENTECH arity:	INC. 82.43%	Conservative:	м
Best Local Similarity: Query Match:	80.41% 35.01%	Mismatches: Indels:	17
rn	DNA; 322 BP.		
DE Human 979636 DNA fi PN WO9914241-A2.	ragment.		
25-MAR-1999. (GETH ) GENENTECH	INC.		
ผ	99.078	Conservative: Mismatches:	0
	34.91%	Indels:	0
502 star W76302	ndard; DNA; 395 BP. DNA fragment.		
WO9914241-A2. 25-MAR-1999.			
(GETH ) GENENTECH rcent Similarity:	INC. 98.18%	Conservative:	0
••	98.18% 34.72%	Mismatches: Indels:	2
RESULT 425 ID ABN74213 standard; DE Bovine embryonic of	cDNA; 1009 BF	CDNA EST #264	
WO200194550-A2.		)    -	
rce at	C. 65.18% 55.80% 33.74%	Conservative: Mismatches: Indels:	21 61 17
RESULT 426 ID AAX37719 standard; DE Human clone T87045	DNA; 293 BP. DNA.		

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Conservative: Mismatches: Indels:	Conservative: Mismatches: Indels: Conservative: Mismatches: Mismatches:	Conservative: Mismatches: Indels:	Conservative: Mismatches: Indels:	Conservative: Mismatches: Indels:	Conservative: Mismatches: Indels: adult brain cI	Conservative: Mismatches: Indels:
PN W09914241-A2.  PD 25-WAR-199.  PA (GETH) GENENTECH INC.  Percent Similarity: 97.94%  Query Match: 31.93%  RESULT 427  ID ACH3092 standard; cDNA; 416 BP.  DE Human testis cDNA #478.  PN US2003073623-A1.  PD 17-ARR-2003.  PA (DRMA/) DRWANAC R T.  PA (LABA/) LABAT I.  PA (STAC/) STACHE-CRAIN B.  PA (STAC/) STACHE-CRAIN B.  PA (LOWE/) JONES I. W	COUNE) JONES D. W.  COULDE) JONES D. W.  St Local Similarity: 91.43%  ETY Match: 30.31%  SULT 428  AAX56528 standard; DNA; 430 BP.  Human R02633 DNA fragment.  W09914241-A2. 25-MR-1999. (GETH ) GENENTECH INC.  rcent Similarity: 82.55%  st Local Similarity: 79.87%	1 standard, DNA; 269 BP. 328920 DNA fragment. 41.A2. 1999. 1899. 18714y: 100.00\$ imilarity: 100.00\$ 2 standard; DNA; 261 BP. 2 standard; DNA; 261 BP.	NC. 100.00\$ 100.00\$ 29.02\$ DNA; 281 BP. Eragment.	NC. 100.00\$ 100.00\$ 28.69\$ DNA; 312 BP. agment.	NC. 97.70% 28.24% CDNA; 1076 BP.	9-A2. 998. GENETICS INST INC. arity: 51.13% milarity: 35.28%

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AAD44660 standard; cDNa; 1022 BP.
Human secreted protein-encoding gene 25 cDNA clone HTEEB42, SEQ ID NO:35.
US2002077287-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein-encoding gene 25 cDNA clone HTEEB42, SEQ ID NO:35.
US2002076756-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Secreted protein-encoding gene 162 cDNA clone HTEEB42, SEQ ID NO:172
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128
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128
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ABZ71351 standard; cDNA; 1022 BP
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PA (HUMA-) HUMAN GENOME SCI INC.

PECCENT Similarity: 50.16*

Beet Local Similarity: 34.19*

Query Match:
                  17-SEP-1998.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC. nt Similarity: 50.16%
PN WO9840483-A2.
PD 17-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI I
Percent Similarity: 50.16%
Best Local Similarity: 34.19%
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Best Local Similarity: 34.19*
28.04*
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Best Local Similarity: 34.19%
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Match: 28.04%
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KYAW H.
FISCHER C L.
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FERRIE A M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENTZ R L.
WEI Y.
MOORE P A.
YOUNG P E.
GREENE J M.
                                                                                                                                                                                                                                                                                   SOPPET D R.
                                                                                                                                                                                                                                                                                                  GENTZ R L. WEI Y.
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ROSEN C A.
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SOPPET D R.
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KYAW H.
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(RUBE/) RUBE
(ROSE/) ROSE
(LIYY/) LI Y
                                                                                                                                                          20-JUN-2002
(RUBE/) RUB
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(LIYY/)
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RESULT 442
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(GENT/)
(WEIY/)
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RESULT 443
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                                                                                                                                                                                                                                                                                                                                                                                                            ACC72652 standard; cDNA; 1197 BP.
Human vascular endothelial junction-associated molecule cDNA,
WO20031025118-A2.
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              ABQ92017 standard; cDNA; 1076 BP.
Human polynucleotide SEQ ID NO 14
US2002065394-A1.
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Percent Similarity: 51.13 
Best Local Similarity: 35.28 
Query Match: 28.17
                                                                                                                                                                                                                                                                    AAS00512 standard; cDNA; 1131 BP.
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RESULT 441
ID AAV34310 standard, DNA, 1022 BP
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Human 2345419 DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX37718 standard; DNA; 250 BP.
Human clone 2345419 DNA.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA; 247 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PA (EOSB-) EOS BIOTECHNOLOGY INC.
Percent Similarity: 51.13%
Best Local Similarity: 35.28%
                                                       30 MAY-2002.
(JACOA) JACOBS K.
(MCCOA) MCCOY J M.
(LAVA) LAVALLIE E R.
(COLL/) COLLINS-RACIE L A.
(ERRA/) EYANS C.
(MERB/) MERBERG D.
(TREA/) TREACY M.
(SPAU/) SPAULDING V.
           1D ABQ32017 standard; cDNA; 10°
DE Human polymucleotide SEQ ID
DE US2002065394-A1.
PD 30-MAY-2002.
PA (MCCO/) MCCOY J. M.
PA (MCCO/) MCCOY J. M.
PA (LAVA/) LAVALIE E. R.
PA (COLL/) COLLINS-RACIE L. A.
PA (EVAN/) EVANS C.
PA (EVAN/) EVANS C.
PA (MREB/) MERBERG D.
PA (TREA/) TREACY M.
PA (SPAU/) SPAULDING V.
PECCENT SIMILARITY: 51.13%
BEST LOCA1 Similarity: 35.28%
QUery MATCh:
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PA (GETH ) GENENTECH INC.

Percent Similarity: 100.00$

Best Local Similarity: 100.00$

Query Match: 28.11$

RESULT 439
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Human 1452523 DNA fragment
WO9914241-A2.
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PD 15-APR-2004.
PA (GETH ) GENENTECH IN Percent Similarity: 5 Best Local Similarity: 2 Query Match: 2
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25-MAR-1999.
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RESULT 435
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RESULT 437
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RESULT 434
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PD 27-I
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RESULT 458
ID AAK94243 standard; CDNA; 1724 BP.
DE Human full-length CDNA, SEQ ID NO: 2844.
PN EP1130094-A2.
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Full length human cDNA clone SeqID 2844.
EP1396543-A2.
                                                                                                                                                                                                                      ADP69032 standard; cDNA; 952 BP.
Human NOV2e encoding cDNA SEQ ID NO:27.
WO2004055158-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADP69034 standard; cDNA; 952 BP.
Human NOV2f encoding cDNA SEQ ID NO:29.
WO2004055158-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP69024 standard; cDNA; 952 BP.
Human NOV2a encoding cDNA SEQ ID NO:19.
WO2004055158-A2.
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DE Full length human cDNA clone SeqI
PN EP1396543-A2.
PD 10-MRA-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 48.38$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA; 1296 BP.
                                                                       BP.
                                                  RESULT 452
ID ADH60143 standard; DNA; 933 B
DE Human JAM 3 DNA.
DE Human JAM 3 DNA.
PN US2003222034-Al.
PD 18-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Percent Similarity: 48.38%
Best Local Similarity: 32.79%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA95306 standard; DNA; 1296
Human CRAM-1 coding sequence.
WO200053749-A2.
                                                                         DNA; 933
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PA (CURA-) CURAGEN CORP.

Percent Similarity: 48.38*

Best Local Similarity: 32.79*

27.46*
   48.38%
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Best Local Similarity: 32.79%
Query Match: 27.46%
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PA (CURA-) CURAGEN CORP.
Percent Similarity: 48.38%
Best Local Similarity: 22.79%
Query Match: 27.46%
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PA (HELI-) HELIX RES INST.
Percent Similarity: 48.3
Best Local Similarity: 32.7
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(CURA-) CURAGEN CORP.
     Percent Similarity:
Best Local Similarity:
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RESULT 453
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RESULT 455
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RESULT 457
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RESULT 454
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Query M
RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABZS8894 standard; cDNA; 933 BP.
Human junctional adhesion molecule 3 (JAM3) encoding cDNA.
WO2003006673-A2.
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Mismatches:
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Human secreted protein-related DNA - SEQ ID 349
WO20030388063-A2.
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Indels:
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Human cDNA from secreted protein gene 25.
US2003225009-A1.
                                                                                                                                                                                                                                                                                                        ADB91286 standard; cDNA; 1022 BP.
Human secreted protein cDNA #SEQ ID 232.
WO2003004622-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-JAN-2003.
(TEXA-) TEXAS BIOTECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                      ID ADB91286 standard; cDNA; 1022 B
DE Human secreted protein cDNA #SE
PN W02003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 50.16%
Query Match:
RESULT 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DE ADC73716 standard; DNA; 1022 BPD BE Human secreted protein-related by WO2003038063-A2.

PD 08-MAY-2003.

PA (HUMA-) HUMAN GENOME SCI INC. Percent Similarity: 50.16% Best Local Similarity: 34.19% Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAL51599 standard; DNA; 897 BP
PA (RUBE) RUBEN S M.
PA (ROSE) ROSEN C A.
PA (LIYY) LI Y.
PA (ZENG) ZENG Z.
PA (KYAW) KYAW H.
PA (FISC) PISCHER C L.
PA (LIHH) LI H.
PA (SOPP) SOPPET D R.
PA (MENY) GENTZ R L.
PA (MOOK) MOORE P A.
PA (GREE) GREENE J M.
PA (GREE) GREENE J M.
PA (FERK) FERRIE A M.
PETCENT SIMILATICY: 50.16%
Best Local Similarity: 34.19%
OUBLY MATCH:
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DE Human junctional adhesion mc
WO2003008541-A2.
PD AC-JAN-2003.
PA (ELIL ) LILLY & CO ELI.
Percent Similarity: 54.84 *
Best Local Similarity: 38.31 *
Query Match: 27.72 *
TRSULT 45
ID ABZ58894 standard; CDNA; 93:0
DE Human junctional adhesion mc
PN WO203006673-A2.
PD A3-JAN-2003.
PA (TEXA-) TEXAS BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENT/) GENTZ R L.
(WEIY) WEI Y.
(WOOR/) WOORE P A.
(YOUN/) YOUNG P E.
(GREE) GREENE A M.
(FERR/) FERRIE A M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ID ADG89762 standard; CD BE Human CDNA from secre PN US2003225009-A1.
PD 04-DEC-2003.
PA (ROSE/) ROSEN C A.
PA (LIYY/) LI Y.
PA (LIYY/) LI Y.
PA (KTAM/) KTAM H.
PA (KTAM/) KTAM H.
PA (FISC/) FISCHER C L.
PA (EDEY/) ABT Y.
PA (SOPP/) SOPPET D R.
PA (SENY/) GENTZ R.
PA (SENY/) GENTZ R.
PA (MOOR/) MOORE P A.
PA (GREE/) RERENE J M.
PA (GREE/) GREENE J M.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (FERR/) HASTINGS G A.
PECCENT SIMILATICY: 34
QUELY MATCH: 28
RESULT 450
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ADG89762 g
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Signature Signature	ABS53477 standard; CDNA; 3554 BP. CDNA encoding human PRO1868 polypeptide. CSC-UOL-2002. (GETH ) GENENTECH INC. (GETH ) GENENTECH INC. St Local Similarity: 48.38\$ Conservative: 48 to Local Similarity: 27.46\$ Indels: 23 Ty March: 27.46\$ Indels: 25 ULT 470 ABL95691 standard; CDNA; 3554 BP.	MOZO0208284-A2. 31-JAN-2002. 31-JAN-2002. GETH) GERENTECH I GEREN/ FERRARA N. (GERB) GERBER H. (GERB) GERBER H. (GODD/) GODDARD N. (GODD/) GODOWSKI P. (GUDV) GODOWSKI P.	WILLIAMS WOOD W I. arity: milarity: standard NA for se NA for se 003. GENENTECH arity:	d; cDNA; 3554 BP. man PRO polypeptide #269. H INC. Conservative: 4 48.38\$ Mismatches: 1 27.46\$ Indels: 2 d; cDNA; 3554 BP. ing secreted/transmembrane protein	Percent Similarity: 48.38% Conservative: 48  Best Local Similarity: 32.79% Mismatches: 137  Query Match: 27.46% Indels: 22  RESULT 474  ID ACH07141 standard; cDNA; 3554 BP.  DE Human secreted/transmembrane polypeptide PRO1868 cDNA.
Best Local Similarity:       32.79\$       Mismatches:       137         Query Match:       27.46\$       Indels:       22         RESULT 460       ID AAK4867 standard; cDNA; 3515 BP.       DE Human full-length cDNA, SEQ ID NO: 4050.         PD BH Human full-length cDNA, SEQ ID NO: 4050.       PD 05-SEP-2001.         PD 05-SEP-2001.       PA (HBLL-) HELIX RES INST.         PA (HBLL-) HELIX RES INST.       Conservative: 48         Percent Similarity: 48.38       Mismatches: 137         Query Match:       27.46\$       Indels:	RESULT 461  ID ADL32017 standard; CDNA; 3515 BP.  DE Full length human cDNA clone SeqID 4050.  PN EP1396543-A2.  PD 10-MAR-2004.  PA (REAS-) RES ASSOC BIOTECHNOLOGY.  Percent Similarity: 32.79% Mismatches: 137  Query Match: 27.46% Indels: 22  TRESULT 462  DAA A1265, standard. CDNA: 3554 BP	DE Human DNA encoding PRO1868, an A33 antigen homologue.  PN WG200036102-A2.  PD 22-JUN-2000.  PA (GETH ) GENENTECH INC.  Percent Similarity: 32.79% Mismatches: 137  Query Match: 27.46% Indels: 22  RESULT 463  ID AACS8622 standard; cDNA; 3554 BP.  DE Human PRO1868 protein UNQ859 encoding cDNA SEQ ID NO:192.  PN WG200053758-A2.  PN WG200053758-A2.  PRESULT 463  RESULT 463  RESULT 463  RESULT 463  RESULT 463  RESULT 623  RES	Standard, cDNA, 3554 BP.  RO1868 cDNA. 4311-A1. GENILA. GENENTECH INC. 1arity: 48.38\$ Conservative: imilarity: 32.79\$ Mismatches: 27.46\$ Indels: 2 standard, cDNA, 3554 BP. DNA sequence encoding for PRO1868 polypept 2001.	PA (GETH ) GENENTECH INC.  Percent Similarity: 48.38\$ Conservative: 48  Best Local Similarity: 32.79\$ Mismatches: 137  Query Match: 27.46\$ Indels: 22  RESULT 466  IN ABS68392 standard; cDNA; 3554 BP.  DE Human cDNA encoding secreted protein PRO1868.  Ph US2002098866-A1.  Ph US2020208866-A1.  PA (GETH ) GENENTECH INC.  Percent Similarity: 48.38\$ Mismatches: 137  Query Match: 27.46\$ Indels: 22  RESULT 467  PRESULT 467	PN US2002098605-A1. PD 25-JUL-2002. PA (GETH ) GENENTECH INC. Percent Similarity: 48.38\$ Conservative: 48  Best Local Similarity: 32.79\$ Mismatches: 137

DD 13-FEB-200 PA (GETH) GE Percent Similar Best Local Simi Query Match: RESULT 483 ID ACA67367 s	CDNA enco US2003032 13-FEB-20	(GETH ) G ccent Simila st Local Sim ery Match:		Grap		.E.S. :	ID ADA46056 s DE Novel huma PN US20030223 PD 30-JAN-200 PD (GETH ) GP		0 ~ 0 0	ccent Similst Local Si st Local Si ery Match:		(GETH ) G cent Simila st Local Sim sry Match:		Cent Simil st Local Si sry Match:	1D ADACION DE Homo sapie PN US20030498 PD 13-MAR-200
48 137 22		48 137 22	protein PRO1868.	48 137 22	#269.	48 137 22		48 137 22		48 137 22	68 cDNA.	48 137 22		48 137 22	tein, SEQ ID 537.
Conservative: Mismatches: Indels:	P. Ypeptide.	Conservative: Mismatches: Indels:	transmembrane	Conservative: Mismatches: Indels:	CDNA	Conservative: Mismatches: Indels:	P. otein cDNA, #63.	Conservative: Mismatches: Indels:	P. otein PRO1868.	Conservative: Mismatches: Indels:	1; cDNA; 3554 BP. transmembrane polypeptide PRO1868	Conservative: Mismatches: Indels:	P. otein cDNA, #7.	Conservative: Mismatches: Indels:	BP. 1/transmembrane pro
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PN US2003044839-A1. PD 06-MR-2003. PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match: RESULT 475	ID ABX11173 standard; cDNA; 3554 BP. DE CDNA encoding human PRO1868 polypeptide PN US2002164646-A1.	PD 07-NOV-2002. PA (GETH ) GENENTECH PETCENT Similarity: Best Local Similarity: Query Match:	RESULT 476 ID ABX89409 standard; of DE DNA encoding novel PN US2003017563-Al.	PD 23-JAN-2003. PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	ACDA2063 standard, CDNA, 3554 BP. DE Human secreted/transmembrane protein (PRO) PN US2003036179-A1.	ន្តិភូមិ	RESULT 478  ID ABX96378 standard; CDNA; 3554 BP. DE Human secreted/cransmembrane protein CDNA, PN US202160374-A1.	PA (GETH ) GENERTECH Percent Similarity: Best Local Similarity: Query March:	RESULT 479 ID ACAGOS699 standard; CDNA; 3554 BP. DE CDNA encoding human secreted protein PRO1868 PN US2003023064-A1.	PA (GETH ) GENETECH Percent Similarity: Best Local Similarity: Query March:	6 standard ecreted / 36060-A1.	g # g	RESULT 481 ID ABX0609 standard; cDNA; 3554 BP. DE Human secreted/transmembrane protein cDNA, PN US2002160392-A1.	PD 31-OCT-Z002.  PA (GETH) GENENTECH Percent Similarity: Best Local Similarity:  Query Match:	KESULT 442 ID 40204292 standard; cDNA; 3554 BP. DE Human cDNA encoding a secreted/transmembrane protein, PN US2003032155-A1.

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standard; CDNA; 3554 BP.
Nan secreted and transmembrane protein PRO1868 CDNA.
463-A1.
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Nan secreted and transmembrane protein PRO1868 cDNA.
1328-A1.
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rreted / transmembrane polypeptide PRO1868 cDNA.
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ding human PRO1917polypeptide.
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O polynucleotide #269.
3212-A1.
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O polynucleotide #269.
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Percent Similarity: 48.38% CC Best Local Similarity: 32.79% M Query March: 27.46% II	encoding human PRO polypeptid 3068794.Al. R-2003. GENENTECH INC. mllarity: Similarity: 32.79\$ Similarity: 746\$	013 standard; CDNA; 3554 BP. human secreted and transmemb. 3082693-A1. Y-2003. I) GENENTECH INC. milarity: 32.79% Similarity: 27.46%	225 standard; cDNA; 3554 BP. PRO polymucleotide #269. 3082705-Al. Y-2003. Milarity: 48.38% Similarity: 32.79%	; cDNA; 3554 BP. leotide #269. INC. 48.38 32.79\$	ADASTORS STANDARY SESSA BP. Novel human secreted and transmemb US2003087345-A1. OB-MAY-2003. (GETH) GENENTECH INC. CCENT Similarity: STY Match: SULT 504	tandard; CDNA; 3554 BP. polynucleotide #269. 33. NENTECH INC. A48.38* Lity: 48.38* Llarity: 27.46*	ACD63512 BEGINDARY 5554 BF. Human PRO Polynuclectide #61. US2003044793-A1. 06-MAR-2003. (GETH ) GENENTECH INC. GETH Similarity: 48.38* St Local Similarity: 32.79* STV Match: 27.46* SULT 506 ADA16458 standard, cDNA, 3554 BP. Human secreted/transmembrane prote US2003049621-A1. 13-MAR-2003. (GETH ) GENENTECH INC.
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Conservative: 48 Mismatches: 137 Indels: 22	II.	vative: ches:	indels: 22 3554 BP.  Lranemembrane protein PRO1868 CDNA.  Conservative: 48 Mismatches: 137	Indels: 22 Conservative: 48 Mismatches: 137		in cDNA, #65. Conservative: 48 Mismatches: 137 Indels: 22	membrane protein PRO1868. Conservative: 48 Mismatches: 22 Indels:
PA (GETH ) GENENTECH INC. Percent Similarity: 48.38* Best Local Similarity: 32.79* Ouery Match: 27.46*	standard; CDNA; 3554 BP. uman secreted and transmemi 68796-Al. 2003. GENENTECH INC. 1arity: 48.38%	27.46% 6 standard; CDNA; 3554 BP. coding human PRO polypeptid 82704-A1. GENENTECH INC. 1arity: 48.38% imilarity: 32.79%	27.46% 5 standard, CDNA; uman secreted and 82711-A1. 2003. GENENTECH INC. 1arity: 48.38% imilarity: 32.79%	27.46% standard; cDNA; 3554 BP. polynucleotide #269. 350-Al. 003. ENENTECH INC. RILLY: 32.79% illarity: 32.79%	1554 BP. 1269.	3 standard; cDNA; 3554 BP. ecreted/transmembrane prote 39971-A1. GD03. GBNENTECH INC. 1arity: 48.38% imilarity: 32.79%	151 standard; cDNA; 3554 BP.  CDNA encoding secreted/trans 3045693-A1.  P. GENENTECH INC.  Similarity: 32.79\$  h: 27.46\$  TO standard; cDNA; 3554 BP.  PRO polynucleotide #269.  RE2003.  GENENTECH INC.

Indels:

27.46%

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137 22	PRO1868 CDNA.	48 137 22		48 137 22	01868 cDNA.	48 137 22		48 137 22	PRO1868 cDNA.	48 137 22		48 137 22	01868 cDNA.	48 137 22	48 137
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Best Local Similarity: Querry Match:	RESULT 50/ ID ADA91962 standard; CDNA; DE Novel human secreted and PN W22003082694-Al.	GUS. GENENTECH arity: milarity:		ξ ;	ACCOUNTY OF THE PROPERTY OF TH	PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	ID ADA94201 standard; cDNA; DE Human PRO polynucleotide PN US2003077722-A1. PD 24-APR-2003	PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Query March:	resoli 311 ID ADB20097 standard; cDNA; DE Novel human secreted and PN US2003082691-A1.	01-MAY-2003. (GETH ) GENENTECH ccent Similarity: it Local Similarity: iry Match:	d;	PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	resolui 213 ID ACD98692 standard; cDNA; DE Novel human secreted and PN US2003044945-A1.	PP 06-MAK-2003. PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Guery Match:	

48 137 22	48 137 22	48 137 22	48 137 22	48 137 22	48 137 22	48 137 22	48 137 22
Conservative: Mismatches: Indels:	Conservative: Mismatches: Indels:	Conservative: Mismatches: Indels:	Conservative: Mismatches: Indels:	Conservative: Mismatches: Indels:	Conservative: Mismatches: Indels: le #269.	Conservative: Mismatches: Indels: ein.	Conservative: Mismatches: Indels:
ard; cDNA; 3554 BP. nuclectide #269. 1. ECH INC. 48.38* ty: 32.79* ard; cDNA; 3554 BP. nuclectide #269.	38% 46% 46% AA; 3554 BP. de #269.	38% 79% 46% 1A; 3554 BP. de SEQ ID NG	38% 79% 46% IA; 3554 BP. de #269.	38% 79% 46% 1A, 3554 BP	ENTECH INC.  ty: 48.38% C.  arity: 32.79% M.  27.46% I.  andard; cDNA; 3554 BP.  ng human PRO polypeptide 6-Al.	INC. 48.38% 32.79% 27.46% DNA; 3554 BP. n PRO1868 protein	INC. 48.38% 32.79% 27.46%
RESULT 523  ID ADA80693 standard; of Human PRO polynuclec PN US2003082761-A1.  PD 01-MAY-2003.  PA (CERT) GENENTECH IP Percent Similarity: Best Local Similarity: RESULT 524  ID ADA75935 standard; of Human PRO polynuclec	PD 01-MAY-2003 PA (GETH ) GENENTECH INC Percent Similarity: 48 Best Local Similarity: 33 Query Match: 27 RESULT 525 ID ADA47160 standard; CI DE Human PRO polynucleot PN US2003073210-A1.	PA (GETH ) GENENY PERCENT SIMILARITY BEST LOCAL SIMILARY QUERY MATCH: RESULT 526 RESULT 526 ED ADB25456 STANC DE HUMAN PRO POLI PHON US203077715-1	PA (GETH) GENENTECH INC. Percent Similarity: 48. Best Local Similarity: 32. Query Match: 27. RESULT 527 ID ADA/93632 standard; CDR DE Human PRO polynucleoti	PD 24-APR-2003. PA (GETH ) GENEWTEC GENEL Similarity: Best Local Similarity: Query Match: RESULT 528 ID ADD26982 standar DE CDNA encoding hu PN US2003092147-A1.	MAY-2003. TH ) GENEN Similarity al Similar tch: 29 31269 stan A encoding 003096386- MAY-2003.	PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match: RESULT 530 ID ACD26813 standard DE CDNA encoding hum PN US2003054447-A1. PD 20-MAR-2003.	PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match: RESULT 531

DE Homo appiens.  PM 520101 94087-2013.  BE Homo appiens.  PM 520103 940817-A1.  PM 520103 94087-2013.  DE 13-WAR-2003.  DESTURY MARCH:  DE HOMO PROPERTIFY: 27.464 Mismacrhes:  PERCENT Similarity: 27.464 Mismacrhes:  DE HOMO PROPERTIFY: 27.464 Mismacrhes:  DE ALARP-2003.  DE HOMO PROPERTIFY: 27.464 Mismacrhes:  DE HOMO PROPERTIFY: 27.464 Mismacrhes:  DESTURY MARCH:  DE HOMO PROPERTIFY: 27.464 Mismacrhes:  DESTURY MARCH:  DE HOMO PROPERTIFY: 27.464 Mismacrhes:  DE HOMO PROPERTIFY: 2
INC.  48.38 32.79 32.77 32.77 32.77 48.38

US2003054351-A1.

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RESULT 544

ID ADA88220 standard; cDNA; 3554 BP.

B Novel human secreted and transmembrane protein PRO1868 cDNA.

BN US2003082700-Al.

PA (GETH ) GENENTECH INC.

Percent Similarity: 48 Mismatches: 137

Query Match: 27.46% Indels: 22
                                                                                                                               ADA87117 standard; cDNA; 3554 BP.
Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003082709-A1.
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Novel human secreted and transmembrane protein PRO1868 cDNA.
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US2003017498-A1.
23-JAN-2003.
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US2003039969-A1.
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US2003049622-A1.
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cDNA encoding human PRO polypeptide #269.
US2003077710-A1.
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(GETH ) GENENTECH INC.
(Cent Similarity: 48.38%
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PD 01-MAY-2003.
PA (GETH) GENEWTECH INC.
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Best Local Similarity: 32.79$
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PD 23-JAN-2203.
PA (GETH) GENENTECH INC.
Percent Similarity: 48.38
Best Local Similarity: 32.79
Query March: 27.46
RESULT 547
                                             GENENTECH INC.
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(GETH ) GENENTECH INC.
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PA (GETH ) GENENTECH INC.

Percent Similarity: 48.

Best Local Similarity: 32.
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PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH IN
Percent Similarity: 3
Best Local Similarity: 3
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                                24-APR-2003
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RESULT 540
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ADA88772 standard; cDNA; 3554 BP.
Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003073213-A1.
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Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003027256-A1.
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Novel human secreted and transmembrane protein PRO1868 cDNA.
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DE CDNA encoding human PRO polypeptide #269.
PN US200302239-A1.
Percent Similarity: 48.38* Conserv
Best Local Similarity: 32.79* Mismatc
                                                                                                         cDNA encoding human PRO polypeptide #269.
US2003082699-A1.
                                                                                                                                                                                                                                               cDNA encoding human PRO polypeptide #269.
US2003082706-A1.
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                                                                                            ADB28638 standard; cDNA; 3554 BP
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US2003082686-Al.
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Percent Similarity: 48.38*
Best Local Similarity: 72.746*
Query Match:
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PA (GETH ) GENENTECH INC.
Percent Similarity: 48.38*
Best Local Similarity: 32.79*
Query Match: 27.46*
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Percent Similarity: 48.3
Best Local Similarity: 32.7
PD 20-MAR-2003.

PA (GETH ) GENENTECH INC.

Percent Similarity: 48.

Best Local Similarity: 32.
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PA (GETH ) GENENTECH INC.
Percent Similarity: 48.
Best Local Similarity: 32.
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Percent Similarity: 48.
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Local Sim / Match: JT 564	ADB66749 standard; Novel human secret: US2003082689-A1. Ol-MAY-2003. (GETH ) GENENTECH	Percent Similarity: Best Local Similarity: Query Match: RESULT 565	ID ADB99829 standard; cDNA; DE Human PRO polynucleotide PN US2003082698-Al. PD 01-MAY-2003. PA (GETH) GENENTECH INC. PA (GETH) GENENTECH 18384 Best Local Similarity: 32.739 Query Match:	KESULI 566 ID ADB90561 standard; DE Human PRO polynucl PN US2003082762-A1. PD 01-MAY-2003. Percent Similarity: Best Local Similarity:	CUCLY MACCH:  RESULT 567  AD ADB77947 standard; cDNA; 3554 BP.  DB Human secreted/transmembrane protein cDNA, PN US2003077654-A1.	PD 24-APR-2003. PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	ADB39662 standard; ADB39662 standard; WOVel human secret; US2003082764-Al.	PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match: RESULT 569	1D ADB75083 standard; cDNA; 3554 BP. DE Human secreted/transmembrane protein PN 01-MAY-2003. PD 01-MAY-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 48.38% Cor Best Local Similarity: 32.79% Mis	KESULT 5 / 0  ID ADB47285 standard  ID B NOVel human secrei  BN US2003082687-A1.  PD O1.MAY-2003.  PA (GETH ) GENENTECH  Best Local Similarity:  Query Match:	TD ADB6692 standard; cDNA; DE Human PRO polymucleotide PN US2003082697-A1. PD 01-MAY-2003. PA (GETH) GENENTECH INC. PA (SETH) GENENTECH INC. PA SIMILARIY: 48.384 Best Local Similarity: 32.793
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Percent Similarity: Best Local Similarity: Query Match:	KESULT 556  ID ACD23852 standard; cDNA; DE Human PRO polynucleotide PN US2003064923-Al. PD 03-APR-2003.	(GETH.) GENENTECH ccent Similarity: st Local Similarity:	8 standard RO polynuc 68793-A1. 2003. GENENTECH larity: imilarity:	RESULT 558  ID ADB23019 standard; CDNA; DE Human PRO polynucleotide PN US200307711-A1. PD 24-APR-2003. PA (GETH) GENENTECH INC. Percent Similarity: 48.38%		يا پير ۾	RESULT 560 ID ADAS214 standard; cDNA; 3554 BP. DE Novel human secreted and transmembrane protein PRO1868 PN US200308212-Al.	ğ # £ £	Journal Strandard and PRO polynuc. 2200308752-A1. J-MAY-2003. SETH ) GENENTECH : Similarity:	9 standard uman secret 82766-Al. 2003. GENENTECH larity: imilarity:	RESULT 563  ID ADB38277 standard; CDNA; DB Novel human secreted and PN US2003087347-A1.  PD 08-MAY-2003.  PA (GETH ) GENENTECH INC.  PA SIMILATILY:  PROFECEL SIMILATILY:  48.388

48 137 22

Conservative: 48 Mismatches: 137 Indels: 22

48 137 22

Conservative: 48 Mismatches: 137 Indels: 22

5	ID ADC39930 standard; cDNA; 3554 BP. DB Human secreted/transmembrane protein cDNA, #65. PN US2003059828-A1.	2 7 E	D ADC4044 standard; cDNA; 3554 BP. DE Human secreted/transmembrane protein cDNA, #65. PN US2003059229-A1.	27-MAR-2003. (GETH) GENENTECH INC. cont Similarity: 48.38% tt Local Similarity: 32.79% xry Match: 27.46%	ID ADC19268 standard; CDNA; 3554 BP. DE Human secreted/transmembrane protein cDNA, #65. PN US2003036661-A1. PD 20-FEB-2003. PA (GETH) GRNENTECH INC. PARCHEL SAMENTECH INC.	ity: 32.79% 27.46%	ID ADC14568 standard; CDNA; 3554 BP. DE Human secreted/transmembrane protein CDNA, #65. PD 20-FEB-2003.	(GEIR ) CENTERLE INC. recert Similarity: 32.73% sty Match: 27.46% SULT 584	ID ADC29623 standard; CDNA; 3554 BP.  DE Human secreted/transmembrane protein CDNA, #65.  PN US2003049676-A1.  PD 13-WAR-2003.  DA (GETH ) CRNEWIFFH INC	Sir at	P. Standard, Cons., 353% br. ecreted/transmembrane prote 49677-A1. GENENTECH INC. 62811ty: 32.79%	Iry Match: SULT 586 ADC41039 standard; Human secreted/trar US2003054400-A1.	PD 20-MAR-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 48.38\$ Conservative: Best Local Similarity: 32.79\$ Mismatches: Query Match: 27.46\$ Indels: RESULT SET	ID ADC19696 standard; cDNA; 3554 BP. DE Human secreted(transmembrane protein cDNA, #65. PN US2003054441-A1. PD 20-MAR-2003. PA (GETH) GENENTECH INC. PARCED Similarity: 48.38% Conservative: Best Local Similarity: 32.79% Mismatches: Query Match: 27.46% Indels:
22	PRO1868 CDNA.	48 137 22		48 137 22		48 137 22		48 137 22 ·		48 137 22		137 22 PRO1868 CDNA.	48 137 22	
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er,	SULT 572 ADB77497 standard; CDNA; Novel human secreted and reconstances.	ar C	4 standard; cDNA; RO polynucleotide	PN USZOBJOTYT7-1.A1. PD 24-APR-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 48.38% Best Local Similarity: 32.79% Query March: 27.46%	8 standard; cDNA; RO polynucleotide 77719-A1. 2003.	rcent Simil st Local Si ery Match:	andard; cDNA; olynucleotide 6-A1.	9 7 G	RESULT 576  ID ADB35206 standard; cDNA; 35  DE Human PRO polynuclectide SE  PN US200307718-A1.	3 4 6	310 standard; cDNA; PRO polynuclectide 8077720-A1. R-2003. GENEWTECH INC. milarity: 48.388	: 32.79% 27.46% d; CDNA; eted and	PN US2003082692-A1. PD 01-MAY-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 48.38* Best Local Similarity: 32.79* Ouery Match: 27.46*	0 standard; ecreted/trai 29772-Al. 2003. GENENTECH I larity: imilarity:

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Conservative: 48 Mismatches: 137 Indels: 22

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ADC54756 standard; cDNA; 3554 BP.
Novel human secreted and transmembrane protein cDNA Seq ID537.
US2003087363-A1.
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Novel human secreted and transmembrane protein cDNA Seg ID537.
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Novel human secreted and transmembrane protein PRO1868 cDNA US2003087367-A1.
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PARCENT SIMILARITY: 48.38%
Best Local Similarity: 32.79%
CHORN MATCH: 27.46%
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Novel human secreted and
US2003087361-A1.
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PA (GETH) GENENTECH INC.

Percent Similarity: 48...

Best Local Similarity: 32.
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PA (GETH ) GENENTECH INC.
Percent Similarity: 48.
Best Local Similarity: 32.
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RESULT 603
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Novel human secreted and transmembrane protein cDNA Seg ID537.
US2003087365-A1.
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US2003087366-A1.
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US2003092106-A1.
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Novel human secreted and transmembrane protein PRO1868
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 ADC34144 standard; cDNA; 3554 BP.
Human secreted/transmembrane protein cDNA, #65.
US2003073077-A1.
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US2003073079-A1.
17-APR-2003.
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ADC57465 standard; cDNA; 3554 BP.
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                                       USACCOST.
17-APR-2003.
(GTH ) GENENTECH INC.
cent Similarity: 48.38$
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Percent Similarity: 48.38%
Best Local Similarity: 32.79%
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PA (GETH ) GENENTECH INC.

Percent Similarity: 48.384

Best Local Similarity: 32.794
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Percent Similarity: 48.
Best Local Similarity: 32.
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PA (GETH ) GENENTECH INC.

Percent Similarity: 48.

Best Local Similarity: 32.
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ID ADC34144 standard; c
DE Human secreted/trans
PN US2003073077-A1.
PD 17-ARR-2003.
PA (GETH ) GENENTECH IN
Percent Similarity: 4
Best Local Similarity: 3
Query Match:
RESULT 589
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PD 17-APR-2003.
PA (GETH ) GENENTECH IN Percent Similarity: 4 Best Local Similarity: 2 Query Match:
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US2003077657-A1.
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Best Local Similarity:
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RESULT 596
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Query Match:
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RESULT 619
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RESULT 614
                                                                                                    ADD03362 standard; cDNA; 3554 BP.
Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003092104-A1.
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Novel human secreted and transmembrane protein PRO1868 CDNA.
US203087354-A1.
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transmembrane protein PRO1868 cDNA.
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Novel human secreted and transmembrane protein PR01868 cDNA, US2003087348-A1.
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CDNA encoding human PRO polypeptide #269.
US2003194770-A1.
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Human PRO polynucleotide #269.
US2003194773-A1.
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Human PRO polynucleotide #269.
US2003194774-A1.
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Human PRO polynucleotide #269.
US2003194776-A1.
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15-MAY-2003.
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fcent Similarity: 48.38%
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PA (GETH ) GENENTECH INC.
Percent Similarity: 48.38*
Best Local Similarity: 27.79*
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PD 08-MAY-2003.
PD (GETH ) GENENTECH INC.
Percent Similarity: 48.38
Best Local Similarity: 32.79
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PD 16-OCT-2003.
PD 46-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 48.38
Best Local Similarity: 32.7'
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PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 48.3
Best Local Similarity: 32.7
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PA (GETH) GENENTECH INC.

Percent Similarity: 48.3

Best Local Similarity: 32.7
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                                                                                               ID ADD03362 standard; c
DE Novel human secreted
PN US2003992104-A1.
PA (GETH) GENENTECH IN
Percent Similarity: 4
Best Local Similarity: 3
Query Match: 2
RESULT 606
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENIECH II
Percent Similarity:
Guery Match:
RESULT 605
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RESULT 611
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ADC80170 standard; cDNA; 3554 BP.

Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003087358-A1.
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Human secreted/transmembrane PRO polypeptide cDNA #131.
US2003105013-A1.
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US2003105011-A1.
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US2003104469-A1.
05-JUN-2003.
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US2003108983-A1.
12-JUN-2003.
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RESULT 618

ID ADD04939 standard, cDNA, 3554 BP. DE Human PRO polynucleotide #269. PN US200319475-A1. PD 16-OCT-2003. PA (GETH) GENENTECH INC. Percent Similarity: 48.38* M Best Local Similarity: 32.79* M
                                                             Query Match:
RESULT 613
TD ADD10550 standard; cDNA; 3554 BP.
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Human PRO polynucleotide #269.
US2003194771-A1.
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ADD03803 standard; cDNA; 3554 BP.
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PD 16-OCT-2003.

PA (GETH ) GENENTECH INC.
Percent Similarity: 48.38*
Best Local Similarity: 27.79$
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PD 08-MAY-2003.
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Best Local Similarity: 32.79%
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PD 05-JUN-2003.
PD 65-TUN-2003.
Percent Similarity: 48.38%
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PA (GETH) GENENTECH INC.

PECCENT Similarity: 48.

PEST Local Similarity: 32.

QUETY MATCH: 27.
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Percent Similarity: 48.
Best Local Similarity: 32.
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RESULT 617
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Percent Similarity: 48.38\$ Conservative: 48 Best Local Similarity: 32.79\$ Mismatches: 137 Query March: 27.46\$ Indels: 22	AESOLI 823 Standard; cDNA; 3554 BP.  ID Novel human secreted and transmembrane protein PRO1868 CDNA. PN US2003203432-A1. PD 30-OCT-2003.	PA (GETH) GENENTECH INC.  Percent Similarity: 48.38\$ Conservative: 48  Best Local Similarity: 32.79\$ Mismatches: 137  Query Match: 27.46\$ Indels: 22  RESULT 630	1554 BP. 1269. Conservative:	ty: 32.79% 27.46% ard; cDNA; 3554 BP.	numan FRO polynicieotide US2003199055-Al. 23-CCT-2003. (GETH ) GENENTECH INC. cent Similarity: 48.38% st Local Similarity: 32.79% EXT MACCH: 27.79%	<pre>ID ADE04181 standard; cDNA; 3554 BP. DE Human PRO Polymucleotide #269. PN US2003199057-A1. PD 23-OCT-2003.</pre>	(GETH ) GENENTECH INC.  CCENT. Similarity: 48.389 st Local Similarity: 32.794 STY Match: 27.469 SULT 633	ADE32478 standard; Novel human secret US2003194765-A1. 16-OCT-2003.	(GETH ) GENENTECH INC. reent Similarity: 48.36 st Local Similarity: 32.73 rry Match: 27.46 sULT 634	DE CDNA encoding human PRO polypeptide #269.  DE CDNA encoding human PRO polypeptide #269.  PN US2003199056-A1.  PD 23-OCT-2003.  PA (GETH ) GENERTECH INC.  Percent Similarity: 48.38 Mismatches: 137  Query Match: 27.46 Indels: 22	ID ADD79634 standard; cDNA; 3554 BP.  DE cDNA encoding human PRO polypeptide #269.  PN US2003203428-Al.  PD 30-OCT 2003.  PA (GETH ) GENETHECH INC.  Percent Similarity: 48.38\$ Conservative: 48  Best Local Similarity: 32.79\$ Mismatches: 137  QUERY MACh: 27.46\$ Indels: 22	ABOUT 3039 Standard; cDNA; 3554 BP.  ID AD942170 standard; cDNA; 3554 BP.  BE Human PRO polynucleotide #269.  PN US203194772-Al.  PD 16-OCT-2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 48.38\$ Conservative: 48
PA (GETH ) GENENTECH INC.  Percent Similarity: 48.38* Conservative: 48  Best Local Similarity: 32.79* Mismatches: 137  Chery Match: 27.46* Tadding	finess: 2 standard; CDNA; 3554 BP. uman secreted and transmembrane protein PR 03438-Al.	PD 30-OCT-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 48.38 Conservative: 48 Best Local Similarity: 32.79% Mismatches: 137 Query Match: 27.46% Indels: 22	; cDNA; 3554 BP. an PRO polypeptide #269. INC.	3 7 7 E	Scandard; CDNA; oding human PRO p 4792-Al. 003. GENEWTECH INC. arity: 48.38% arity: 22.79%	cDNA; 3554 BP. ed and transmembrane protein PF	CT-2003. H ) GENENTECH INC. imilarity: 48.381 1 Similarity: 32.791 ch: 27.461	Į,	PD 05-JUN-2003. PA (GENEWIECH INC. PA (GENEWIECH INC. Percent Similarity: 48 Conservative: 48 Best Local Similarity: 32.79* Mismatches: 137 Charry Match: 27.46* Indels: 22	A ADD51939 standard; cDNA; 3554 BP.  DE CDNA encoding human PRO polypeptide #269.  PN US2003194779-A1.  PD IG-OCT-2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 48.38* Conservative: 48  Physical Similarity: 77.46* Tridial.	8 standard; CDNA; 3554 BP. RO polynucleotide #269. 03431-A1. GENENTECH INC. Conservative: 4 imilarity: 48 38* Tudala: 77 46* Tudala: 1	standard; cDNA; 3554 BP. RO polynucleotide #269. 2003. GENENTECH INC.

Best Local Similarity: Query Match:	32.79% 27.46%	Mismatches: Indels:	137 22	Query Match: RESULT 645
RESULT 637 ID ADE17987 standard; c	CDNA; 3554 BP.			ID ADE19091 standa DE Human PRO polyn
99023-A1. 2003.	- + × × × × × × × × × × × × × × × × × ×			
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Dest Local Similarity: Query Match:	32./98 27.468	Mismarcnes: Indels:	13/ 22	Query Match: RESULT 646 TD ADE43287 standa
standard; O polynucle	cDNA; 3554 BP.			DE Human PRO polyn US2003199033-A1
PN US2003199053-A1. PD 23-OCT-2003.	=			PD 23-OCT-2003. PA (GETH ) GENENTE
	NC. 48.38%	Conservative:	48	rcent Simil
milarity:	32.79%	Mismatches: Indels:	137	Query Match: RESULT 647
standard	CDNA: 3554 BP.			ID ADD96076 standa DE Human PRO polyn
		transmembrane protein PRO1868	RO1868 CDNA.	US200319
003. Genentech	Ö.			PA (GETH ) GENENTE Percent Similarity:
arity:	48.38%	Conservative:	48	Best Local Similarit
Best Local Similarity: . Query Match:	32.79 <b>*</b> 27.46 <b>*</b>	Mismatches: Indels:	137 22	Query Match: RESULT 648
4 standard	CDNA: 3554 BP.			ID ADE22962 standa
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(GETH ) GENENTECH . cent Similarity:	NC. 48.38*	Conservative:	48	Percent Similarity: Best Local Similarit
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RESULT 642			44	3
ID ADD93223 standard; or Human PRO polynucled	cDNA; 3554 BP. otide #269.			DE Novel human sec
PN US2003194768-A1.				
PD 16-OCT-2003. PA (GETH ) GENENTECH IN	INC.			PA (GEIH ) GENENIE Percent Similarity:
	48.38%	Conservative:	4.8	Best Local Similarit
Similatity: h:	27.46%	Indels:	13/ 22	QUEIY MALCH: RESULT 651
5	CDNA: 3554 BD			ID ADE42722 standa
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				PD 23-OCT-2003.
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imilarity:	32.79%	Mismatches:	137	Query Match:
ory march: SULT 644	27.46\$	indels:	22	KESULT 652 ID ADD80738 standa
d; rar	cDNA; 3554 BP.	ein cDNA, #65.		
US2003077583-A1. 24-APR-2003.				PD 06-NOV-2003. PA (GETH ) GENENTE
(GETH ) GENENTECH :	INC. 48.38%	Conservative:	8	Percent Similarity: Best Local Similarit
τy:	32.79%	Mismatches:	137	Query Match:

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27.46%	ALBISOUR SCHROLAGE CONA; 3534 BF. Human PRO polynucleotide #269. US2003199026-A1. 23-OCT-2003. (GETH) GENENTECH INC. GETH) GENENTECH INC. st Local Similarity: 48.38% ery Match: 27.46% ADE43287 standard; CDNA; 3554 BP. Human PRO polynucleotide #269.	03200137035 A1. 23-0CT-2003. (GETH ) GENENTECH INC. ccent Similarity: 48.38\$ srt Local Similarity: 32.79\$ sry Match: 27.46\$ srur 6A ADD96076 standard: CDNA: 355	COLNA; 3534 B Sectide #269. INC. 48.38% 32.79%	F22962 standard; cDNA; 3554 BP. NA encoding human PRO polypeptic 1200199064-A1CCT-2003. FETH ) GENENTECH INC. Similarity: 48.38% cal Similarity: 32.79% fatch: 27.46%	080 standard; cDNA; 3554 BP. encoding human PRO polypepti 3203429-Al. T-2003. ) GENENTECH INC. Allarity: 48 38 Similarity: 27.46 h:	O standard, CDNA, 3554 BP.  Uman secreted and transmemt 2003.  GENENTECH INC. 1arity: 48.38 imilarity: 27.79\$ imilarity: 27.76\$	RESULT 651  ID ADE42722 standard; CDNA; 3554 BP. DE Human PRO polynucleotide #269. PN US2003199032-A1. PD 23-CCT-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 48.38* Best Local Similarity: 32.79* Query Match: 27.46*	652 B80738 standard; CDNA; 3554 BP. NA encoding human PRO polypeptic 2003207418-A1NOV-2003. ETH ) GENENTECH INC. Similarity: 48.38% cal Similarity: 27.79%

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ADG23328 standard; cDNA; 3554 BP.
Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003207384-A1.
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Novel human secreted and transmembrane protein PRO1868 cDNA.
US20032073355-A1.
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US2003194777-A1.
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                                                                                                                         Human PRO polynucleotide #269. 032003199031-Al.
RESULT 653
ID ADD89766 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003199028-A1.
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Human PRO polynucleotide #269.
US2003207370-A1.
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PA (GETH ) GENENTECH INC.
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PA (GETH) GENENTECH IN Percent Similarity:
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ADE04849 standard;
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Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003207381-A1.
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Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003207385-A1.
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Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003207386-A1.
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Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003207387-A1.
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ADH59538 standard; cDNA; 3554 BP.
Human secreted/transmembrane protein cDNA, #65
US2003039972-A1.
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 ADG80175 standard; cDNA; 3554 BP.
Human PRO polynucleotide #269.
US2003207372-A1.
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rcent Similarity: 48.38%
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Percent Similarity: 48.38%
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PA (GETH ) GENENTECH INC.

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ID ADG80175 standard; cb Human PRO polymuclec PN US2003207372-A1. PD 06-NOV-2003. PA (GEHT) GENENTECH IN Percent Similarity: 3 Best Local Similarity: 3
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ADH55467 standard;
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Novel human secreted and tra	GG-NOV-2003. (GETH) GENENTECH INC. Int Similarity: 48.38* Match: Similarity: 32.79*	8 standard; cDNA; 3 uman secreted and t 07377-A1.	(GETH ) GENENTECH INC. int Similarity: 48.38* Local Similarity: 32.79* Match: 27.46*	7 standard; cDNA; 35 RO polynucleotide #6 46709-A1. 2002. GENEYTECH INC.	1cy: 32./9% 27.46% dard; cDNA; 3 ecreted and t	PD 05-DEC-2002. PA (GETH ) GENENTECH INC. PA (GETH ) GENENTECH INC. Best Local Similarity: 3-79% Query Match: 27.46%	RESULT 673  ID ACA66977 standard, cDNA, 3554  DE CDNA encoding human secreted p  PN US2002192668-A1.	19-DEC_2002. (GETH) GENENTECH INC. cent Similarity: 48.38% t Local Similarity: 32.79% ry Match: 27.46%	RESULT 6.74  ID ACD24121 standard; cDNA; 355  DE Novel human secreted and tre  PN US2003032156-A1.  PD 13-FEB-2007	im / GENENADOR 1NC. imilarity: 48.38\$ 1 Similarity: 32.79\$ Ch: 27.46\$	CDNA PRO INC.	imilarity: 32.77 27.44 2 standard; cDNA coding human PRO	H INC. 48.38\$ : 32.79\$ 27.46\$ d; cDNA; 3
DE Nove	rce Bt ery	ID ADH810 DE NOVEL PN US2000	9 9 4 6	KESULI 6/1 ID ACA5925 DE HUMAD PEN US20021 PD 10-OCT- PA (GETH ) Percent Simi	Best Local Signature Control Street Match: RESULT 672 ID ACA6408 DE Novel Participation Treet Match Street	PD 05-D PA (GET Percent S Best Loca Query Mat	RESULT 67 ID ACA6 DE CDNA PN US20	PD 19-D PA (GET Percent S Best Loca Query Mat	RESULT 67 1D ACD2 DE Nove PN US20 PD 13-F	Percent S Percent S Best Loca Query Mat RESULT 67	ID ACAS DE CDNA PN US20 PD 19-D PA (GET	Best Local S Query Match: RESULT 676 ID ACA6726 DE CDNA en	PD 02-JAN PA (GETH Percent Sim Best Local Query Match RESULT 677

Human PRO1868 CDNA.

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DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 48.38* Conservative: 48
Best Local Similarity: 32.79$* Mismatches: 137
Query Match: 27.46$* Indels: 22
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Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003087356.A1.
(GB-MAY-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003087357-A1.
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Novel human secreted and transmembrane protein PRO1868 cDNA. US2003087353-A1.
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Novel human secreted and transmembrane protein PRO1868 cDNA.
US2003087385-A1.
08-MAY-2003.
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transmembrane protein PRO1868 cDNA.
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Human secreted/transmembrane protein cDNA, #65.
US2003135025-A1.
                                                                                                                    AD226585 standard; cDNA; 3554 BP.
Human secreted/transmembrane protein cDNA, #65
US2003054349-A1.
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PD 08-MAY-2003

PA (GETH ) GENENTECH INC.
Percent Similarity: 32.798

Best Local Similarity: 27.468
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DE Human secreted/transmembrane
DD 10-MAR-2003
PA (GETH ) GENENTECH INC.
PA (GETH ) GENENTECH INC.
PACIFIC Similarity: 48.38*
Best Local Similarity: 32.79*
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RESULT 680

ID ADN16116 standard; CDNA; 35:

DE Novel human secreted and tre

PN US2003087353-A1.

PD 08-MAY-2003.

PA (GETH) GENEWICH INC.

Percent Similarity: 48.38%

Best Local Similarity: 27.9%

Query Match:

RESULT 681
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Percent Similarity: 48.38*
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Percent Similarity: 48.38*
Best Local Similarity: 32.79*
Query Match: 27.46*
RESULT 683
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Novel human secreted and
US2003092115-A1.
PN US2003170864-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 48.
Best Local Similarity: 32.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.

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INC. 48.38% 32.79% 27.46%	cDNA, 3554 BP. ectide #269. INC. 48.38* 32.79* 27.46*	cotide #269.  ectide #269.  INC. 48.38\$ 27.46\$  CDNA, 3554 BP.  ectide #269.	INC. 48.38% 32.79% 27.46% CDNA; 3554 BP.	INC. 48.38% 32.79% 27.46% cDNA, 3554 BP.	INC. 48.38 32.79 27.46\$	; cDNA; 3554 BP. insmembrane protein INC. 48.38\$ Cor 32.79\$ Mis	
PD 17-JUL-2003. PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	DE ADD76722 standard; cDNA; DB Human PRO polynuclectide PN US2003100087-A1. PD 29-MAY-2003. PA (GETH ) GENENTECH INC. PROFILE INC. PROF	RESULT 687  ID ADD8086 standard; cDNA; 3  DE Human PRO polynuclectide #  PN US2030302113-A1.  PD 15-MAY-2003.  PA (GETH) GENENTECH INC.  Percent Similarity: 48.38   Best Local Similarity: 32.79   Query Match: 27.98   RESULT 688  RESULT 688  ID ADD86490 standard; cDNA; 3  DE Human PRO polynucleotide #	PD 02-0CT-2003. PD 30-0CT-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 48.38\$ CCO GUEST MACCH: 22.79\$ Mit RESULT 689 ID ADET79924 standard; CDNA; 3554 BP. DE Human secreted/transmembrane protein PN US2003130489-A1.	grafit Grafit	PN USZ003211571-A1. PD 13-NOV-2003. PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	0 standard ecreted/tr 29592-Al. 2003. GENENTECH larity: imilarity:	S11 standard; secreted/tra 3100497-A1. 3100497-A1. 51-2003. 51-31-31-31-31-31-31-31-31-31-31-31-31-31

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Human secreted/transmembrane protein cDNA, #65.
US2003211576-A1.
(GETH ) GENENTECH INC.
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Human secreted/transmembrane protein cDNA, #65
US2003148370-AI.
                                                                                                                                                                                                                ADE24709 standard; cDNA; 3554 BP.
cDNA encoding human PRO polypeptide #269.
US2003092111-A1.
                                                                         ADE24066 standard; cDNA; 3554 BP.
CDNA encoding human PRO polypeptide #269.
32003092110-A1.
15-MAY-2003.
(GETH ) GENENTECH INC.
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RESULT 697
ID ADEB9400 standard; CDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003199062-A1.
PD 23-OCT-2003.
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DE Human PRO polynucleotide #269.
PN US2003194794.Al.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 48.38% COMBEST LOCAL Similarity: 27.46% IRESULT 700
                                                                                                                                                                                                                                                                                                                                                          ADD87534 standard; cDNA; 3554 BP.
Human PRO polynucleotide #269.
US2003203439-A1.
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Human PRO polynucleotide #269.
US2003199054-A1.
                                                                        D ADE24066 standaru, ......, DE CDNA encoding human FRO polyp DE CDNA encoding human FRO polyp D 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 48.38*
Best Local Similarity: 32.79*
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DE Human secreted/transmembrane
DE Human secreted/transmembrane
DO 07-803148370-AI.
PA (GETH ) GENENTECH INC.
PACETH ) GENENTECH INC.
PACETH Similarity: 48.38*
Percent Similarity: 32.79$*
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PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 48.38%
Best Local Similarity: 32.79%
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PD 23-OCT-2003,
PA (GETH ) GENENTECH INC.
Percent Similarity: 48.38%
Best Local Similarity: 32.79%
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Best Local Similarity: 32.79%
Query Match: 27.46%
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(GETH ) GENENTECH INC.
PA (GEIN, J. Percent Similarity:
                                Best Local Sir
Query Match:
RESULT 694
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RESULT 695
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RESULT 701
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RESULT 699
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RESULT 698
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Mismatches: 137 Indels: 22 3554 BP.	cein Froisco Live: 48 es: 22	BP. protein cDNA, #65. Conservative: 48 Mismatches: 137 Indels: 22	protein cDNA, #65.	Conservative: 48 Mismatches: 137 Indels: 22 BP. protein CDNA, #65.	Conservative: 48 Mismatches: 137 Indels: 22	Conservative: 48 Mismatches: 137 Indels: 22 3554 BP. transmembrane protein PRO1868 CDNA.	Conservative: 48  Mismatches: 137  Thels: 22 3554 BP.	Conservative: 48 Mismatches: 137 Indels: 22
32.79% 27.46% CDNA;	DE NOVEL NUMBER SECTETE AND LIBER NOVEL NUMBER NUMB	ST S	DE Human secreted/transmembrane prot pro 18200325253-A1.  PD 04-DEC-2003.  PA (GDDD/) GODDARD A.  PA (GDDD/) GODDARD A.  PA (GDDV/) GODWART P J.  PA (MATH/) MATHER J P.  PA (WILL/) WILLIAMS P M.  PA (WILL/) WILLIAMS P M.	cent Similarity: st Local Similarity sty Match: SULT 713 Human secreted/ US2003180312-A1	PD 25-SEP-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 48.38% Best Local Similarity: 32.79% Query Match: 27.46% RESULY 714 ID ADG02453 standard; CDNA; 3554 DE Human PRO Polynucleotide #269. PN US2003207352-A1.	06-NOV-2003. (GETH) GENENTECH INC. ccent Similarity: 48.389 st Local Similarity: 32.799 ETY MATCH: 27.464 ADG22239 standard; CDNA; Novel human secreted and	PN US2003207360-A1. PD 06-NOV-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 48.38* Best Local Similarity: 32.79* Query Match: 27.46* RESULT 716 ID ADG20309 standard; CDNA; 3554 BP DE CDNA encoding human PRO polypept PN US2003207376-A1.	SUL SUL
48 137 22	48 137 22	48 137 22	48 137 22	48 137 22			ዋጸ	84
48.38\$ Conservative: 32.79\$ Mismatches: 27.46\$ Indels:	CDNA; 3554 BF.  PRO polypeptide #269.  INC. 48.38\$ Conservative: 27.46\$ Indels:	cDNA; 3554 BP. sotide #269. INC. A8.38\$ Conservative: 32.79\$ Mismatches: 27.46\$ Indels:	cDNA; 3554 BP.  PRO polypeptide #269.  INC. 48.38 Conservative: 27.46% Indels:  CDNA: 3554 BP.	# 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	CDNA, 3554 BP.  1 PRO polypeptide #269.  INC.  Conservative: 32.79\$ Mismaches: 77.46\$ Thdels:	CDNA; 3554 BP.  smembrane protein CDNA, #65.  INC.  COMBETVALIVE:  32.79\$  Mismatches:	Indels: 3554 BP. transmembrane protein Conservative: Mismatches: Indels:	3554 BP. #269.
rce st ery SUI	EB94868 standard; NA encoding human 2003199027-A1. -OCT-2003. ETH ) GENENTECH : Similarity: cal Similarity:	RESULT 703  ID ADE91279 standard; CDNA; ID Human PRO polynucleotide PN US2003199061-A1. PD 23-OCT-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 32.794 QUETY MAtch: PERCHT 704 PERCHT 704	0 standard; coding human 29052-Al. 2003. SENENTECH J larity: imilarity:	Human PRO polynucle US2003199060-A1. 23-OCT-2003. (GETH ) GENENTECH I rcent Similarity: Et Local Similarity:	standard; coding humar 99029-Al. 2003. GENENTECH I larity: imilarity:	8 standard; ecreted/trai 11569-A1. 2003. GENENTECH : larity:	Query Match:  RESULT 708  ID ADE92426 standard; cDNA;  DE Novel human secreted and  PN US2003199051-A1.  PD 23-CAT-2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 48.389  Best Local Similarity: 32.799  Query Match:	7 standard; RO polynucle 99063-A1. 2003. GENENTECH :

PN US2003166051-A1. PD 04-SEP-2003. PA (GETH ) GENBRITCH INC. Percent Similarity: 32.79\$ Mismatches: 137 Query Match: 27.46\$ Indels: 22	ID ADG13486 standard; cDNA; 3554 BP.  DB cDNA encoding human PRO polypeptide #269.  PN US2003207357-A1.  PD 06-NOV-2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 48.38* Conservative: 48  Best Local Similarity: 32.79* Mismatches: 137  Query Match: 27.46* Indels: 22	RESULT 727  ID ADG08543 standard; CDNA; 3554 BP.  DE Novel human secreted and transmembrane protein PRO1868 CDNA.  PN US2003207424-A1.  PD 06-NOV-2003.  PA (GETH) GENENTECH INC.  Percent Similarity: 48.38* Conservative: 48  Best Local Similarity: 27.46* Indels: 22	standard; CDNA; coding human PRO I 19885-Al. 2003. GENENTECH INC. 1arity: 48.384 imilarity: 27.468	ID ADF97111 standard; cDNA; 3554 BP.  DE Human PRO polynucleotide #269.  PN US200320731-A1.  PD 06-NOV-2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 48.38\$ Conservative: 48  Best Local Similarity: 27.79\$ Mismatches: 137  Query Match: 27.46\$ Indels: 22  RESULT 730	ADG06296 standard; cDNA; Human PRO polymucleotide US2003207374-A1. 06-NOV-2003. (GETH ) GENENTECH INC. (GETH ) GENENTECH INC. 31 Local Similarity: 48.38% sty Match: 27.79%	ADG21880 standard; cDNA; 3554 Novel human secreted and trans US2003207389-A1. 06-NOV-2003. (GETH ) GENENTECH INC. rcent Similarity: 48.38% sty. Match: 27.46% SULT 732.	DE Human PRO polymucleotide #269.  DE Human PRO polymucleotide #269.  PN US2003207423-A1.  PD 06-NOV-2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 48.38* Conservative: 48  Best Local Similarity: 32.79* Mismatches: 137  Query Match: 27.46* Indels: 22  RESULT 733  ID ADG25070 standard; cDNA; 3554 BP.  DE Novel human secreted and transmembrane protein PRO1868 CDNA.  PN US2003207427-A1.
8 3.77 3.77	PRO1868 CDNA. 48 137	2 8 37	2 88 	8 37 2	8 3.7 2	8 37 2	8 37
Conservative: 4 Mismatches: 1 Indels: 2	protein rvative: tches:	, " U 4H	Indels: 2 Conservative: 4 Mismatches: 1 Indels: 2	Conservative: 4 Mismatches: 1 Indels: 2	#269. nnservative: 4 smatches: 1	Conservative: 4 Mismatches: 1 Indels: 2	tive: 4 es: 1 2 #65.
DE Human PRO polynucleotide #269. PN US203307422-A1. PD 06-NOV-2003. PA (GETH) GENEWECH INC. Percent Similarity: 48.38% Best Local Similarity: 72.46%	2 standard; CDNA; uman secreted and 07426-A1. 2003. GENENTECH INC. 1arity: 32.79%	6 standard RO polynuc 08055-A1. 2003. GENENTECH larity: imilarity:	n: 617 standard; 1 PRO polynucle 320731-A1. 7 GENENTECH I milarity: 5 Similarity:	RESULT 721  ID ADF99338 standard; CDNA; 3554 BP.  BE Human PRO polynucleotide #269.  PN US2003207353-A1.  PD 06-NOV-2003.  PA (GETH) GENENTECH INC.  Percent Similarity: 48.38%  Percent Similarity: 43.79%  Query Match: 27.46%	standard, coding humar coding humar 2003. GENENTECH J larity: imilarity:	RESOLT 723  ID ADG05382 standard; CDNA; 3554 BP. DE Human PRO polynucleotide #269. PN US2003207375-A1. PD 06-NOV-2003. PA (GETH) GENENTECH INC. Percent Similarity: 48.38* Best Local Similarity: 32.79* Query Match: 27.46*	ID ADG19649 standard; cDNA; 3554 BP.  DE CDNA encoding human PRO polypeptide #269.  PN US2003207425-A1.  PD 06-NOV-2020.  PA (GETH) GENENTECH INC.  Percent Similarity: 48.38* Mismatch Query Match: 27.46* Indels:  RESULT 725  ID ADF73675 standard; cDNA; 3554 BP.  DE Human secreted/transmembrane protein cDNA,

Percent Simi Best Local S Query Match: RESULT 742	DE NOVEL PO 1970/1970/1970/1970/1970/1970/1970/1970/	Percent Simi Percent Simi Best Local S Query Match:	1D ADG5599 DE Novel P PN US20032 PD 06-NOV-	Percent Simi Percent Simi Best Local S Query Match: RESULT 744	1D ADG5872 DE NOVEL P PN USZ0032 PD 06-NOV-	PA (GETH ) Percent Simi Best Local Covery Match 1 RESULT 7456	DE MOVELLE DE NOVELLE PN US20032 PD 06-NOV	PA (GETH ) Percent Sim Best Local Query Match	,,,,,	Stry Stry	1D ADGS817 DE NOVG1 P PN US20032 PD 06-NOV	E S	DB NOVEL 17 DB NOVEL 17 DB NOVEL 17 DP 06-NOV- PA (GET) PA CALL 17 PACCELT SIMIL BEST LOCAL SIMIL RESULT MATCH: RESULT MATCH: TD ADG7164	DE Novel P PN US20032 PD 06-NOV-
48 137 22	PRO1868 CDNA.	48 137 22	PRO1868 CDNA.	48 137 22	PRO1868 CDNA.	48 137 22	PRO1868 CDNA.	48 137 22	PRO1868 CDNA.	48 137 22		48 137 22	48 137 22 `	RO1868 cDNA.
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INC. 48.38% 32.79% 27.46%	cDNA; ed and	INC. 48.38% 32.79% 27.46%	and	INC. 48.38% 32.79% 27.46%	cDNA; ed and	INC. 48.38% 32.79% 27.46%	NA; and	INC. 48.38% 32.79% 27.46%		INC. 48.38% 32.79% 27.46%	cDNA; 3554 BP nsmembrane pro	INC. 48.38% 32.79% 27.46%		
PA (GETH) GENERACH Percent Similarity: Best Local Similarity: Query Match:	DE Novel human secreted and PN US2003207350-A1.	Ub-NOV-2003. (GETH) GENENTECH ccent Similarity: tt Local Similarity: xry Match:	KESULT 735 ID ADG07919 standard; CI DE Novel human secreted PN US2003207356-A1.	Ub-NOV-2003. (GETH ) GENENTECH CCORT Similarity: It Local Similarity: ITY Match:	KESULT 736 ID ADG55414 standard; cDNA; DE Novel human secreted and PN US2003194778-A1.	16-OCT-2003. (GETH ) GENENTECH Cent Similarity: tt Local Similarity: rry Match:	ID ADG61078 standard; cl DE Novel human secreted PN HS2001207390-A1	06-NOV-2003. (GETH ) GENENTECH cent Similarity: of Local Similarity: rry Match:	RESULT 738  ID ADG62182 standard; cDNA; DE Novel human secreted and PN US2003207428-A1.	06-NOV-2003. (GETH) GENENTECH cent Similarity: tt Local Similarity: rry Match:	RESULT 739  ID ADG92518 standard; cDNA; 3554 BP.  E Human secreted/transmembrane protein cDNA, PN US2003027145-A1.	1 t i	RESULT 740  DE Human PRO polymclectide PN US2003207358-A1. PA (GFTH) GENENTECH INC. PA (GFTH) GENENTECH INC. Percent Similarity: 48.384 Query Match: 27.7464 RESULT 74.1	ID ADG57622 standard; cDNA; DE Novel human secreted and PN US2003207362-A1.

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758 standard, cDNA, 3554 BP.
human secreted and transmembrane protein PRO1868 cDNA.
3207415-A1.
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human secreted and transmembrane protein PRO1868 cDNA.
3207363-A1.
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human secreted and transmembrane protein PRO1868 CDNA.
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i) GENENTECH INC.
conservative: 48
milarity: 48.38* Mismacrches: 137
similarity: 32.79$* Indels: 22
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human secreted and transmembrane protein PRO1868 cDNA.
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                                                                         070 standard; cDNA; 3554 BP. human secreted and transmen 3207364-A1.
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7H ) GENENTECH INC.

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7,15 21,15	gr tr g	ID ADMAS71 DE Human P PN US20030 PD 30-JAN- PA (GETH) Percent Simi Best Local S Query Match: RESULT 760	1D ADG5486 DE Novel h PN US20032 PD 06-NOV- PA (GETH ) Percent Simi	NESULY 761 RESULY 761 ID ADG5990 DE NOVEL P PN US20032 PD 06-NOV-	g t y E	ID ADH2073 DE Human 6 DN US20040 PD 08-JAN-1	9 7 7 5	Siry at G	1D ADH0758 DE Human 8 PD PD 08-JAN-		PA (WODD/) PA (WODD/) Percent Simi. Best Local S. Query Match:
48 137 22	48 137 22	137 22	PRO1868 CDNA.	22 22 PRO1868 CDNA.	48 137 22	PRO1868 CDNA.	48 137 22	48 137 22	PRO1868 CDNA.	48 137 22	PRO1868 CDNA.
Conservative: Mismatches: Indels:	Conservative: Mismatches: Indels:	Conservative: Mismatches: Indels:	3554 BP. transmembrane protein Pl Conservative:	. 4	Conservative: Mismatches: Indels:	3554 BP. transmembrane protein Pi	Conservative: Mismatches: Indels:	Conservative: Mismatches: Indels:	3554 BP. transmembrane protein PF	Conservative: Mismatches: Indels:	3554 BP. transmembrane protein PF
48.38% 32.79% 27.46%	cDNA; 3554 BP. sotide #269. 48.38% 27.46%	; cDNA; 3554 BP. leotide #269. INC. 48.38% 32.79% 27.46%			INC. 48.38% 32.79% 27.46%		INC. 48.38% 32.79% 27.46%	; cDNA; 3554 BP. lectide #269. INC. 48.38% 32.79% 27.46%		INC. 48.38% 32.79% 27.46%	
Percent Similarity: Best Local Similarity: Query Match: PRSHT 760	ID ADG81831 standard; cDNA; 3554 DE Human PRO polynucleotide #269 PN US2003207865-A1. PD 06-NOV-2003. Percent Similarity: 48.38% Best Local Similarity: 32.79%	93 standard PRO polynuc: 077723-A1. 1-2003. ) GENENTECH illarity: Similarity:	0 standard uman secrei 07419-A1. 2003. GENENTECH larity:		003. GENENTECH arity: milarity:		PD 06-NOV-2003. PA (GETH) GENENTECH I Percent Similarity: Best Local Similarity: Query Match:	9 standard RO polynuc 94793-A1. 2003. GENENTECH larity: imilarity:	KESULI 756 ID ADG56518 standard; cDNA; DE Novel buman secreted and PN US2003207366-A1.	06-NOV-2003. (GETH ) GENENTECH : ccent Similarity: st Local Similarity: sry Match:	4 standard; uman secret 07378-A1. 2003.

Indels: 22 3554 BP. transmembrane protein PRO1868 cDNA.	Conservative: 48 Mismatches: 137 Indels: 22 P.	Conservative: 48 Mismatches: 137 Indels: 22	1354 BP.  transmembrane protein PRO1868 cDNA.  Conservative: 48 Mismatches: 137 Indels: 22	1554 BP.  transmembrane protein PRO1868 cDNA.  Conservative: 48  Mismatches: 137  Indels: 22	BP. protein cDNA, #65. Conservative: 48 Mismatches: 137 Indels: 22	Conservative: 48 Mismatches: 137 Indels: 22 P.	
PA (GETH ) GENENTECH INC. Percent Similarity: 48.38% Best Local Similarity: 32.79% Ouery Match:	NA; 3554 B	30-JAN-2003. (GTTH ) GENEWTECH INC. recent Similarity: 48.38% st Local Similarity: 27.46% SULT 760	2 standard; CDNA; man secreted and 07367-A1. 2003. GENEWTECH INC. 1arity: 32.79% imilarity: 32.79%	ADG59902 standard, cDNA, Novel human secreted and US2003203303369-A1. 06-NOV-2003. (GETH ) GENENTECH INC. crent Similarity: 48.38% st Local Similarity: 27.9% STY Match: 27.46% SULT 762	734 standard; cDNA; 3554 8ecreted/transmembrane 4005553-A1. N-2004. ) GENENTECH INC. milarity: 48.38% Similarity: 32.79%	4 standard; CDNA; 3554 B RO polynucleotide #131. 24084-Al. 2003. GENENTECH INC. 1arity: 32.79* imilarity: 37.46* 9 standard; CDNA; 3554 B ecreted (fransmembrane prof671-Al.	G C

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Best Local Similarity:
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Novel human secreted and transmembrane protein PRO1868
US2004009548-A1.
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Novel human secreted and transmembrane protein PRO1868
US2003207382-A1.
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Human secreted/transmembrane protein cDNA, #65.
US2003096340-A1.
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US2003190610-A1.
US-CCT-2003.
(GETH) GENENTECH INC.
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CDNA encoding human PRO polypeptide #269.
US2003207361-A1.

06-NOV-2003.

(GETH ) GENENTECH INC.

CECH Similarity: 48.38*

Conservat.

CLocal Similarity: 32.79*

Indels:
                                                                                                                        Human secreted/transmembrane protein cDNA, US2004005665-A1.
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PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 48.38%
Best Local Similarity: 32.79%
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PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 48.38$
          PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 48.
Best Local Similarity: 32.
Ouery Match:
                                                                                                                                                                       (DESN/) DESNOYERS L. (GODD/) GODDARD A. (GODO/) GODOWSKI P J. (GURN) GURNEY A L. (MATH/) MATHER J P. (WILL/) WILLIAMS P M. (WOOD/) WOOD W I.
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(GETH ) GENENTECH INC.
                                                                                                          ID ADH07162 standard; c
BE Human secreted/trans
PN US2004005655-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODD/) GODDARD A.
PA (GURN/) GURNER J P.
PA (WILL/) WILLIAMS P M.
PA (WILL/) WILLIAMS P M.
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Percent Similarity: 3
Best Local Similarity: 3
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ADG09417 standard; cDNA; 3554 BP.
Novel human secreted and transmembrane protein PRO1868 cDNA.
US2004009547-A1.
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US2003207349-A1.
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US2003207383-A1.
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RESULT 778
ID ADJ99851 standard; CDNA; 3554 BP.
BB. Human secreted/transmembrane protein CDNA, #65.
PN US2003187238-A1.
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US2003186358-A1.
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US2004023331-A1
   Mismatches:
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Human PRO1868 cDNA from DNA77624-2515 clone.
US2003228664-Al.
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ID ADH60794 standard; cDNA; 3554 BP
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ID ADM25385 standard; cDNA; 3554 BP
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DD 02-OCT-2003.
PD 02-OCT-2003.
PAR (GETH) GENENTECH INC.
PARCENT Similarity: 48.38%
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(GODO/) GODOWSKI P J.
(GURN) GURNEY A L.
(MATHA) MATHER J P.
(WILL/) WILLIAMS P M.
(WODD/) WOOD W I.
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PA (GETH ) GENENTECH INC.
Percent Similarity: 48.
Best Local Similarity: 32.
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(DESN/) DESNOYERS L.
                                                                                        PD 15-JAN-2004.
PA (GETH) GENENTECH |
Percent Similarity:
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RESULT 775
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RESULT 779
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RESULT 777
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PN USG686451-B1. PD 03-FEB-2004. PA (GETH ) GENENTECH INC. Percent Similarity: 48.38% Best Local Similarity: 32.79% Query Match: 27.46%	SULT 789 ADM28487 standard; CDNA encoding hume US2004077064-A1.	PA (GETH) GENENTECH INC. Percent Similarity: 48.38% Best Local Similarity: 32.79% Query Match: 27.46%	ID ADKI1309 standard; cDNA; 3554 FDE Human secreted/transmembrane property US2004137561-A1. PD 15-UUL-2004. PA (GETH) GENENTECH INC. Percent Similarity: 48.38% Best Local Similarity: 32.79% Query March:	ADR18218 standard, Human secreted/tra US2004147017-A1. 29-JUL-2004. (ASHK/) ASHKENAZI (BOTS/) BOTSTEIN D (DESN/) DESNOYERS (EATO/) EATON D L.	(FILV, PILVAROF (FONG), FONG S. (GAOW), GAO W. (GERR), GEREER H (GERR), GERRITSEE (GODD), GODDARD (GODO), GODDARD (GRIN), GURNALDI (GRIN), GURNEEY A		(WOOD) WOOD WITH THE SIMILATION OF THE SULL TYPE SULL TYPE AD195969 STANDARD CSDN encoding hum US2003077659-A1.	rcent Simi. st Local S. ery Match: SULT 793 AD19652. Novel hu US20032 06FTH ) rcent Simi.
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ansmembrane protein cDNA, INC. 48.38 Conserva	cDNA;	INC. 48.38\$ 32.79\$ 27.46\$	; CDNA; 3554 BP ansmembrane pro INC. 48.38 32.79\$	; cDNA; 3554 BP lectide #269. INC. 48.38 27.46\$	cotide #131. lectide #131. INC. 48.38 27.76\$	i CDNA; 3554 BP.  INC. 48.38% Mismat 27.79% Indels	in PRO polypeptide #269 INC. 48.38\$ Conser 32.79\$ Mismat 27.46\$ Indels	cDNA, 3554 BP.  In PRO polypeptide #269  INC. 48.38* Conser 32.79* Mismat 27.46* Indels cDNA, 3554 BP.
screted/tr. 96233-A1. 1003. GENENTECH arity: milarity:	Query match: RESULT 781 ID ADJ63748 standard; DE Novel human secrete PN US2004039164-A1.	PD 26-FEB-2004. PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Query Match:		RESULT 783  ID ADJ77643 standard; ID Human PRO polymucl PN US2004038336-A1. PD 26-FEB-2004. PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity:	RESULT /84 ID ADK83039 standard, ID Human PRO polynuc] PN US20004043927-A1. PD 04-MAR-2004. PA (GETH ) GENENTECH Perroent Similarity: Best Local Similarity: Query Match:	RESOLIT 785 ID ADJ65765 standard; DE CDNA encoding huma PN US2004038335-A1. PD 26-FRB-2004. PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Desting 266	1D ADM37901 standard; DE CDNA encoding huma PN US2004048333-A1. PD 11-MAR-2004. PA (GETH ) GRNENTECH Percent Similarity: Best Local Similarity: RESULT 737	625 standard encoding hum 4058424-A1. 4058424-A1. 7058121 ) GENENTECH milarity: Similarity: h: 457 standard; PRO polynuci

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SUI SUI SUI SUI SUI	and the second s	RESULT 797  10 ARQ5499 standar  10 Human ovarian an  PN W0200200677-A1.  PD 03-JAN 2002.  PA (HUMA-) HUMAN GE  Percent Similarity.  Best Local Similarity.  Query Match:	

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Human secreted protein-related DNA - SEQ ID 625.
W02003038063-A2.
08-MAY-2003.
                                                                                                         ADC73991 standard; DNA; 4385 BP.
Human secreted protein-related DNA - SEQ ID 624.
MOZ003038663-AZ.
08-MAZ-2003.
                                                                                                                                                                                                                                                              ADD37816 standard; cDNA; 4385 BP.
Human secreted protein encoding sequence #298.
WO200290526-A2.
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DE Human secreted protein gene 13 clone HAPSA79.

PD 19-0CT-2000.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (HUMA-) HUMAN 32.794 Mismatches:

Query Match:

27.464 Indels:
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Human secreted protein gene 13 clone HAPSA79.
WO200061623-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                  ADA56717 standard; DNA; 4385 BP.
Gene encoding human secreted protein #592.
WO2002102994-A2.
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RESULT 806

ID AAR72837 standard; DNA; 4386 BP.

DE Secreted protein gene #39.

PN WO200107459-A1.

PD 01-FEB-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Percent Similarity: 48.38*

Query Match: 27.46*

RESULT 807

ID ADC73992 standard; DNA; 4386 BP.

DE Human secreted protein-related DNA PN WO2003038063-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID AAF72811 standard; DNA; 4386 BP.
DE Secreted protein gene #13.
DW WO20107459-A1.
DD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 48.38%
Best Local Similarity: 32.79%
Query Match:
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ID ADC73991 standard; DNA; 4385 BP
DE Human secreted protein-related 19

BN W02003038063-A2.

PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity:

Regt Local Similarity:

RESULT 801
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DE Human secreted protein encoding
PN W0200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 48.38%
Query Match:
RESULT 802
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RESULT 804
ID JAAC69575 standard; DNA, 4386 BP DE Human secreted protein gene 13
PN W020061633-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 48.38%
Query Match:
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 48.38*
Best Local Similarity: 32.79*
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(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                 ID ADAS6717 standard, DNA; 438E
DE Gene encoding human secreted
PN W020210294-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC
Percent Similarity: 48.38%
Best Local Similarity: 32.79%
Query Match: 27.46%
RESULT 803
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RESULT 805
ID AAF728
DE Secret
PN WO2001
PD 01-FEB
PA (HUMA-
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Conservative: Mismatches: Indels: NA - SEQ ID 401.	Conservati Mismatches Indels:	sequence #299.  Conservative: Mismatches: Indels: .	Conservative: Mismatches: Indels: BP. protein #592.	Conservative: Mismatches: Indels: Lein #592.	Conservative: 4 Mismatches: 1 Indels: 2 IP. cDNA, SEQ ID NO:106	Conservative: Mismatches: Indels: Pp.	Conservative: Mismatches: Indels:
PA (HUMA-) HUMAN GENOME SCI INC. Percent Similarity: 48.38% Guest March: 27.46% RESULT 808 ID ADC73768 standard; DNA; 4386 BP. DE Human secreted protein-related DNA PN WO2003038063-A2.	NOME SCI INC. 48.38 32.79 27.46 d; CDNA; 4386 BP	Human secreted protein encoding WO200290526-A2. 14-NOV-2002. (HUMA-) HUMAN GENOME SCI INC. reent Similarity: 48.38% st Local Similarity: 32.79% st Local Similarity: 32.79% sur. Match: 27.46% SULT 810 ADD37720 standard; cDNA; 4386 BP Human secreted protein encoding WO200290526-A2.	14-NOV-2002. (HUMA-) HUMAN GENOME SCI INC. reent Similarity: 48.38 % st. Local Similarity: 32.79 % SULT 811	rce st ery SUL	(HUMA) HUMAN GENOME SCI INC. Crent Similarity: 48.38 tocal Similarity: 32.79 total String Match: 27.46 total SULT 813 total Su	U4-AFR 2002.  (HUMA.) HUMAN GENOME SCI INC. rcent Similarity: 48.38% Exp. Local Similarity: 27.78% STUT 814 AAC7423 standard; cDNA; 3560 B Human secreted protein gene 15 WO200056754-Ai.	PD 28-SEP-2000.  PD 28-SEP-2000.  Percent Similarity: 48.05%  Best Local Similarity: 32.79%  Query Match: 27.40%  RESULT 815  ID AAX56535 standard; DNA; 387 BP.  DE Human AA152150 DNA fragment.  PN W0991444-A2.  PD 25-MAR-1999.  PA (GETH) GENENTECH INC.

	, o	50 131 25		47 138 22		0 11 0		000		48 131 22	it (huJAM2sv) cDNA.	50 129 37	50 132 14	
Conservative: Mismatches: Indels:	SEQ ID NO: 20	Conservative: Mismatches: Indels:	ng sequence.	Conservative: Mismatches: Indels:		Conservative: Mismatches: Indels:		Conservative: Mismatches: Indels:	BP. VEJAM (NOJAM) CDNA	Conservative: Mismatches: Indels:	2 splice variant	Conservative: Mismatches: Indels:	Conservative: Mismatches: Indele:	Conservative:
100.00% 100.00% 27.20%	coding sequence	50.32% 34.39% 27.17%	cDNA; 1956 BP. noglobulin coding	RM INC. 48.05% 32.79% 27.14%	DNA; 252 BP. fragment.	INC. 96.43% 96.43% 27.07%	DNA; 260 BP. fragment.	INC. 100.00% 100.00% 27.01%	cDNA, 1389 variant of	50.81% 35.28% 26.98%	cDNA; 972 BP.	ELI. 48.92% 33.54% 26.88%	cDNA; 1940 BP.  19 sequence #2.  NE SA.  SO.68\$ 26.88\$	cDNA; 1943 BP. ng sequence #1. sNE SA. 50.68\$
Percent Similarity: Best Local Similarity: Obery Match:	818 NH98352 standard; Jman EST-derived D200154477-A2.	02-AUG-2001. (HYSE-) HYSEQ INC. nnt Similarity: Local Similarity: Match:	LI 81, AAA27386 standard; cDNA; 1 Human IGFAM-6 immunoglobul WO200029583-A2.		25 standard; 1932979 DNA 241-A2.	R-1999.  ) GENENTECH   milarity:  Similarity:  h:	KESULI 819 ID AAXS6517 standard; DE Human 3236257 DNA 9 PN W09914241-A2.	K-1999. ) GENENTECH milarity: Similarity: h:	RESULT 820 ID AAL60897 standard; of the Human novel splice 'PN WO2003046180-A2. PD 05-JUN-2003.	PA (GEST) GENSET SA. Percent Similarity: Best Local Similarity: Query Match: PREMIT 921	standard; ction adh 058-A2.		4484647	LT 8295304 standard; CDN Murine CRAM-1 coding E WOZGO053749-A2. 14-SEE-2000 (RMPD-) RMF DICTAGENE ENT SIMILARITY:
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33.78% 26.88%	cDNA; 3717 BP. Itially expressed	49.16% 33.11% 26.88%	CDNA; 1295 BP.	NC.	50.85% 35.15% 26.42%	DNA; 1295 BP. A clone DNA35638-1141	.NC.	50.85% 35.15% 26.42%	CDNA; 129	6155W0 11	NC.	35.15% 26.42%		cDNA; 1295 BP. .n encoding cDNA,	INC.	50.85% 35.15%	26.42%	DNA; 1295 BP.		INC. 50.85%	35.15% 26.42%	CDNA; 1295 BP.	* in	35.15% 26.42%	CDNA; 1295 BP.	INC.	50.85% 35.15%
Best Local Similarity: Query Match:	KESULI 824 ID ACHO4172 standard; CDNA; DE Human CDNA differentially PN US2003065157-A1. PD 03-APR-2003.	PA (LASE/) LASEK A W. Percent Similarity: Best Local Similarity: Ouery Match:	AESOLI 023 ID AAX37664 standard; DE Human PRO245 CDNA. PN W09914241-A2.	PD 25-MAR-1999. PA (GETH ) GENENTECH 1	Percent Similarity: Best Local Similarity: Query Match:	RESULT 826 ID AAX52225 standard; ID Protein PRO245 cDNA	FN MOSSI4328-A2. PD 25-MAR-1999. PA (GETH ) GENENTECH 1	Percent Similarity: Best Local Similarity: Chark Match:	RESULT 827 ID AAC58586 standard; DE Himan DBO345 nrotei	PN WO200053758-A2. PD 14-SEP-2000.	PA (GETH ) GENENTECH ]	Best Local Similarity: Onerv Match:	RESULT 828	ID AAZ52202 standard; cDNA; 1295 DE Human PRO245 protein encoding PN WO200015797-A2.	PD 23-MAR-2000. PA (GETH ) GENENTECH 1	Percent Similarity: Rest Local Similarity:	Query Match: RESULT 829	ID AAA77562 standard; c DE Human PRO245 cDNA se	PN WO200032221-A2. PD 08-JUN-2000.	PA (GETH ) GENENTECH 1 Percent Similarity:	Best Local Similarity: Query Match: Decir 230	DE ADC78383 standard; DE Human PRO245 CDNA. PN WO200015796-A2.	23-MAR-2000. (GETH ) GENENTECH	Best Local Similarity: Query Match:	KESULI 831  ID AAF72383 standard; DE Human PRO245 cDNA.	I	Percent Similarity: Best Local Similarity:

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AAC97437 standard; cDNA; 1295 BP.
Human angiogenesis-associated protein PRO245 cDNA, SEQ ID NO:90.
WO200053753-A2.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2002197671-A1.
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18.200213240-A1.
19.5EP-2002.
(GETH ) GENENTECH INC.
ir 832
AASO0157 standard; cDNA; 1295 BP.
Human cDNA clone DNA35638-1141 encoding PRO245 (UNQ219).
WO200119991-A1.
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Human cDNA for secreted/transmembrane protein PRO245.
US2003003530-A1.
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Mismatches: 128
Indels: 16
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Human CDNA sequence encoding for PRO245 polypeptide.

Human CDNA sequence encoding for PRO245 polypeptide.

WOZ00140466-A2.

07-JUN-2001.

(GETH ) GENENTECH INC.

Cent Similarity: 50.85$

Conservative: 46

t Local Similarity: 35.15$

Indels: 126
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ACA03770 standard; CDNA; 1295 BP.
CDNA encoding human PRO polypeptide #168.
CDNA encoding human PRO polypeptide #168.
CONSENSOR 182003.
CONSENSOR 18.
CGFTH ) GENERATECH INC.
Excent Similarity: 50.85% Conservat ercent Similarity: 35.15% Mismatche watch: 26.42% Indels:
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AAC91463 standard; CDNA; 1295 BP.
Human PRO245 cDNA.
WC200073452-A2.
07-DEC-2000.
(GETH ) GENENTECH INC.
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                                                            22-MAR-2001.
(GETH ) GENENTECH INC.
cent Similarity: 50.85%
st Local Similarity: 35.15%
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(GETH ) GENENTECH INC.
cent Similarity: 50.85$
t. Local Similarity: 35.15$
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ent Similarity: 50.85$

Local Similarity: 35.15$

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Local Similarity: 35.15%
Match: 26.42%
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ID ACA54860 standard; cDNA; 1295 BP.  DE Novel human secreted and transmembrane protein PRO245 cDNA.  PN US2003017463-A1.  PD 23-JAN-2003.  PA (GETH) GENENTECH INC.  Percent Similarity: 50.85* Conservative: 46  Best Local Similarity: 35.15* Mismatches: 128  Query Match: 26.42* Indels: 16	RESULT 845 Standard; CDNA; 1295 BP.  DE Human secreted / transmembrane polypeptide PRO245 cDNA.  PN US2003027143-A1.  PN 04-FFR-2013	(GFTH) GENENTECH INC. cent Similarity: 50.85% t. Local Similarity: 35.15% STY Match: 26.42%	ID ADA45854 standard; cDNA; 1295 BP.  DE Novel human secreted and transmembrane protein PRO245 cDNA.  PN US2003022328-A1.  PD 30-JAN-2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 50.85% Conservative: 46  Best Local Similarity: 35.15% Mismatches: 128	1017 B31 ADA76285 standard; CDNA; 1295 BP. Human PRO Polynucleotide #168. USA08103212-A1. 17-APR-2003.	PA (GETH ) GENENTECH INC.  Percent Similarity: 50.85\$ Conservative: 46  Best Local Similarity: 35.15\$ Mismatches: 128  Query Match: 26.42\$ Indels: 16  RESULT 852 erandard: CDNA: 1295 RD	INC. 50.85% 25.15% 26.42%	ADA18935 standard; cDNA; 1295 Human PRO polymucleotide #168 US2003054517-A1. 20-MAR-2003. (GETH ) GENENTECH INC. (GETH ) GENENTICY: 50.85\$ sty Match: 26.42\$ ULT 854	DE Homo sapiens.  DE Homo sapiens.  PN US2003049816-A1.  PD 13-MAR-2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 35.15% Mismatches: 128  Query Match: 26.42% Indels: 16  RESULT 855	ID ADB19343 standard; cDNA, 1295 BP.  DE Novel human secreted and transmembrane protein PRO245 cDNA.  PN US2003068796-A1.  PD 10-APR-2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 50.85% Conservative: 46  Best Local Similarity: 35.15% Mismatches: 128  Query Match: 26.42% Indels: 16  RESULT 856  ID ADB27884 standard; cDNA, 1295 BP.
2 standard; cDNA; 1295 BP. ecreted/transmembrane polyp4439-A1. GRNS. GRNEWTECH INC. larity: 50.85* imllarity: 35.15*	Indels: 1295 BP. ed and transmembrane pro	rce ery	.295 BP. ine prote	26.42% Indels: 26.42% Indels: ; cDNA; 1295 BP. ansmembrane protein cDNA, #13.	PD 31-OCT-2002.  PA (GETH ) GENEWIECH INC.  Percent Similarity: 50.85% Conservative: 46  Best Local Similarity: 35.15% Mismatches: 128  Query Match: 26.42% Indels: 16	ID ACA05390 standard, CDNA, 1295 BP.  DE CDNA encoding human secreted protein PRO245.  PN US200320364-A1.  PD 30-JAN-2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 50.85\$ Conservative: 46  Best Local Similarity: 35.15\$ Mismatches: 128  CONSERVATION: 164	7 standard; cDNA; 1295 BP. 2003. 2003. GENERATECH INC. 1arity: 50.85\$ Conservative: 4 imilarity: 35.15\$ Mismatches: 1 indels: 1	KESULY 846  ID ABX93348 standard; CDNA; 1295 BP.  DE CDNA encoding human A-33 related antigen PRO245.  PN US2002182206-A1.  PD 05-DEC-2002.  PA (GETH ) GENENTECH INC.  Percent Similarity: 50.85\$ Conservative: 46  Best Local Similarity: 35.15\$ Mismatches: 128  Ouerv Match: 26.42\$ Indels: 16	1 standard; CDNA; 1295 BP. DNA encoding a secreted/transmembrane prot 2003. GENENTECH INC. CENENTECH INC. As 150.85* Conservative: imilarity: 35.15* Indels:

US2003082693-A1.

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4 1 2 8 1 2 8	PRO245 cDNA.	46 128 16	46 128 16	46 1128 16		46 128 16	protein PRO245.	46 128 16	46 128 16		46 128 16	RO245 cDNA.
de #168. Conservative: Mismatches: Indels:	protein	Conservative: Mismatches: Indels:	Conservative: Mismatches: Indels:	Conservative: Mismatches: Indels:	ein cDNA, #13.	Conservative: Mismatches: Indels:	smembrane prote	Conservative: Mismatches: Indels:	Conservative: Mismatches: Indels:	de #168.	Conservative: Mismatches: Indels:	1295 BP. transmembrane protein PRO245
encoding human PRO polypeptide 3082704-Al. Y-2003. ) GENENTECH INC. milarity: 50.85\$ CA Similarity: 26.42\$ In	cDNA; 1295 BP. ed and transmembrane	INC. 50.85% 35.15% 26.42%	cotide #168. INC. 50.85\$ 26.42\$	cDNA; 1295 BP. ectide #168. INC. 50.85\$ 26.42\$	cDNA; 1295 BP. nsmembrane protein	INC. 50.85% 35.15% 26.42%	cDNA; 1295 BP. g secreted/transmembrane	INC. 50.85% 35.15% 26.42%	coulde #168. lectide #168. INC. 50.85% 26.42%	cDNA; 1295 BP. n PRO polypepti	INC. 50.85% 35.15% 26.42%	
DE CDNA encoding huma: PN US2003082704-A1. PD 01-MAY-2003. PA (GETH) GENENTECH Percent Similarity: Query Match:	standard; man secret		standard, O polynuc] 7350-Al. 003. GENENTECH arity: milarity:	RESULT 859  RESULT 859  ID ADA4713 standard; CDNA;  DE Human PRO polynucleotide  N US2003073215-A1.  PD 17-APR-2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 50.85;  Best Local Similarity: 35.15;  Query Match:	ULT 860 ADA18124 standard; cDNA; 1295 Human secreted/transmembrane p	FN 0.22003.039971-A1. PD 27-FEB-2003. PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match: RESULT A61	ID ACD66842 standard; o DE Human cDNA encoding PN US2003045693-A1.	.003. GENENTECH arity: milarity:	standard O polynuc] 8795-A1. 003. GENENTECH arity: milarity:	RESULT 863 LD ADB30515 standard; CDNA; 1295 BP. DE CDNA encoding human PRO polypeptide PN US2003068794-A1.	003. GENENTECH arity: milarity:	.T 864 ADA85811 standard; cDNA; Novel human secreted and
DE CDI PN US: PD 01: PA (G) Percent Best Loc	RESULT ID ADI DE NO	PD 01 PA (G) Percent Best Lo	KESULT ID AD DE Hu PN US PD 08 PA (G PA (G PERCENT BEST LO	RESULT ID AD DE HU PN US PD 17 PA (G Percent Best LO	RESULT ID AD DE HU	PN US PD 27 PA (G Percent Best Lo Query M	ID AC DE Hu PN US	PD 06 PA (G Percent Best Lo Query M	KESULT 862 ID ADA675 DE HUMAN PN US2003 PD 10-APR PA (GETH PETCENT SIM BEST LOCAL QUERY MATCH	RESULT ID AD DE CD PN US	PD 10 PA (G Percent Best Lo Query M	RESULT 864 ID ADA85

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ID ADA79327 standard; cunn, ....

ID ADA79327 standard; cunn, ....

BE Human PRO polynucleotide #168.

PN US2003082763-A1.

PD 01-MAY-2003.

PA (GETH ) GRNENTECH INC.

Percent Similarity: 50.85* Conservative: 46

Best Local Similarity: 26.42$ Indels: 128

Query Match: 26.42$ Indels: 16

RESULT 867

ID ADA87466 standard; cDNA; 1295 BP.

DE Novel human secreted and transmembrane protein PRO245 cDNA.

PN US200308734-A1.

PN US200308734-A1.

PN GGETH ) GENENTECH INC.

PRAY-2003.

PA (GETH ) GENENTECH INC.

Percent Similarity: 50.85$ Conservative: 46

Best Local Similarity: 26.42$ Indels: 16
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PD 01-MAY-2003.
PA (GETH ) GENETECH INC.
Percent Similarity: 50.85$ Conservative: 46
Best Local Similarity: 35.15$ Mismatches: 128
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Human secreted/transmembrane protein cDNA, #13.
US2003049621-A1.
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DE Human PRO polynucleotide #168.

DO 98-MAY-2003

PA (GETH ) GENENTECH INC.

Percent Similarity: 50.85% Misser Match:

RESULT 869

DB Human PRO polynucleotide #11.

PN US2003044793-A1.

PD 06-MAR-2003

PA (GETH ) GENENTECH INC.

CC Percent Similarity: 35.15% Inc.

DB Human PRO polynucleotide #11.

PD 06-MAR-2003

PA (GETH ) GENENTECH INC.

Percent Similarity: 50.85% Misser Local Similarity: 26.42% Inc.

RESULT 870:
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Human PRO polynucleotide #168.
US2003087351-A1.
                                                                                                                                                                                                     BP.
                                                                                                                                                                                              ID ADA97023 standard; cDNA; 1295 BPDE Human PRO polynucleotide #168.
PN US2003082705-A1.
PD O1-MAY-2003.
PA (GETH) GENEWTECH INC.
Percent Similarity: 50.85$
Best Local Similarity: 35.15$
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PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 50.85
Best Local Similarity: 35.15
Query Match: 26.42
RESULT 865
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PN US2003049621-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

PEST (GETH) GENENTECH INC.

Best Local Similarity: 50.85

Best Local Similarity: 26.42

RESULT 871

ID AAA91760 standard; CDNA, DE NOVEL human secreted and US200308294-A1.

PD 01-MAY-2003.
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RESULT 866
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PA (GETH) GENENTECH INC. Percent Similarity: 50.85\$ Conservative: 46 Best Local Similarity: 35.15\$ Mismatches: 128 Query Match: 26.42\$ Indels: 16 RESULT 881 ID ADA82218 standard; cDNA; 1295 BP. DE Human PRO Polynucleotide #168. PN US2003082701-A1. PD 01-MAY-2003.	20.85\$ Conservative: 35.15\$ Mismatches: 26.42\$ Indels: 1 cDNA; 1295 BP. 1ectide #168. INC. 50.85\$ Conservative:	in PR	7 standard; cDNA; 1295 uman secreted and trans 82708-A1. 2003. GENENTECH INC. 1arity: 50.85\$ imilarity: 35.15\$	ID ACD23181 standard; cDNA; 1295 BP.  DE Human PRO polynucleotide #11.  PN US2003064367-A1.  PD 03-APR-2003.  PA (GETH) GENENTECH INC.  Percent Similarity: 50.85\$ Conservative: 46  Best Local Similarity: 35.15\$ Mismatches: 128  Query Match: 26.42\$ Indels: 16  RESULT 866  RESULT 866  RESULT 867  TH AND2963 standard: CDNA: 1295 RP.	CDNA encoding human PRO polyper US2003073214-A1. 17-APR-2003. (GETH) GENEWTECH INC. cent Similarity: 50.85% st Local Similarity: 35.15% sty Match: 26.42% NULT 887 ADA80491 standard; CDNA; 1295	DE Human PRO POLYNICIEOLIGE #108.  PN US200308761-A1.  PD 01-MAY-2003.  PA (GETH) GENENTECH INC.  Percent Similarity: 55.08\$
PD 08-MAY-2003.  PA (GETH) GENENTECH INC.  Percent Similarity: 50.85\$ Conservative: 46  Best Local Similarity: 35.15\$ Mismatches: 128  QUETY MATCH: 26.42\$ Indels: 16  RESULT 873  ID ADB18784 standard; cDNA; 1295 BP.  PN US2003732121-AI.  PD 17-APR-2003	H Cd;	reerent Similarity: st Local Similarity: sry Match: sury Match: sury Match: ADB19895 standard, Novel human secret US2003082691-A1. 01-MAY-2003. (GETH ) GENENTECH rcent Similarity: st Local Similarity:	7 standard; CDNA; 1295 BP. RO polynuclectide #168. 2003. GENENTECH INC. 1arity: 55.85% Conservative: 4 imilarity: 35.15% Indels: 1	RESULT 877  ID ACD98531 standard; CDNA; 1295 BP.  DE Novel human secreted and transmembrane protein PRO245 CDNA.  DE Novel human secreted and transmembrane protein PRO245 CDNA.  PN US2003044945-A1.  PD 06-MAR-2003.  PA (GETH) GENENTECH INC.  Percent Similarity: 50.85\$ Mismatches: 128  Query March: 26.42\$ Indels: 16	ID ADA74461 standard; cDNA; 1295 BP.  DE Human PRO polynucleotide #168.  PN US2003068798-A1.  PD 10-APR-2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 50.85\$ Conservative: 46  Best Local Similarity: 35.15\$ Mismatches: 128  Query Match: 26.42\$ Indels: 16	DE Human georeted/transmembrane protein cDNA, #13.  DE Human georeted/transmembrane protein cDNA, #13.  PN US2003054401-A1.  PD 20-MAR-2003.  PA (GETH) GENENTECH INC.  Percent Similarity: 50.85\$ Mismatches: 128  Query March: 26.42\$ Indels: 16  RESULT 80  ID ADB24694 standard; cDNA; 1295 BP.  DE Human PRO polymucleotide SEQ ID NO 335.  PN US2003077713-A1.

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Best Local Similarity: Query Match: RESULT 897 ID ADA81043 standard; DE Human PRO polynucle PN US2003082702-A1.	01-MAY-2003.  (GETH ) GENENTECH (GETH ) GENENTECH st Local Similarity:  ary Match: SULT 898 HUMBO PRO polynuci US2003082759-A1.	State	OLI-MAY-2003.  (GETH) GENENTECH cent Similarity: it Local Similarity: sty Match: SULT 900 ADB21713 standard; US2003082765-A1.	01-MAY-2003. (GETH) GENENTECH cent Similarity: st Local Similarity: sty Match: sty Match: Human PRO polynuci Human PRO polynuci US2003068797-A1. 10-APR-2003. (GETH) GENENTECH cent Similarity: sty Match:	ID ADB18232 standard; CD DB CDNA encoding human F W US200307710-A1.  PD 24-ARR-2003.  PA (GETH ) GENENTECH INC GETH Similarity: 50 Best Local Similarity: 35 Query Match: 26 RESULT 903  RESULT 903  ID ADA86915 standard; CD DE NOVED human secreted PN US2003082709-A1.	PD 01-MAY-2003.  Per (GETH ) GENERTECH INC. Percent Similarity: 50.85% Best Local Similarity: 35.15% Query Match: 26.42% RESULT 904 DB Human secreted/transmembrane DB Human secreted/transmembrane PD 27-FEB-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 50.85% Best Local Similarity: 35.15%
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Query Match:	ACCOUNT JOSS TO TOWN, 1295 BP.  ID ADA12952 standard; CDNA; 1295 BP.  DE Human secreted/transmembrane protein CDNA, PN US2003049622-A1.	PD 13-MAR-2003. PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	RESULT 906 ID ADA41820 standard; cDNA; 1295 BP. DE Human secreted/transmembrane protein cDNA, PN US2003082540-A1.	9 7 5	RESULT 907 ID ADA88018 standard; cDNA; DE Novel human secreted and PN US2003002700-A1.	PD 01-MAY-2003. PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	RESULT 908  ID ADA46406 standard; cDNA; DE Novel human secreted and PN US2003054516-A1.	003. GENENTECH arity: milarity:	ID ADA17167 standard; CDNA; 1295 BP. DE Human secreted/transmembrane protein CDNA,	PD 23-JAN-2003. PA (GETH) GENENTECH PErcent Similarity: Best Local Similarity: Query Match:	RESULT 910  ID ADA42670 standard; cDNA; 1295 BP. DE Human secreted/transmembrane protein cDNA,	PD 20-MAR-2003. PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	2	PD 01-MAY-2003. PA (GTTH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	RESULY 912 D ADB28988 standard; CDNA; 1295 BP. DE CDNA encoding human PRO polypeptide #168 PN US2003082706-A1.	S T F

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38570 standard; cDNA; 1295 BP.

11 human secreted and transmembrane protein PRO245 cDNA.
003073213-Al.

ARR-2003.

IH ) GENENTECH INC.

Similarity: 50.85$ Conservative: 46

Similarity: 35.15$ Mismatches: 128

cch: 26.42$ Indels: 16
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Human PRO polynucleotide SEQ ID NO 335.
6940 standard; cDNA; 1295 BP.
n PRO polynucleotide #168.
03059909-A1.
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n PRO polynucleotide #168.
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ETH ) GENENTECH INC.

Similarity: 50.85$

ocal Similarity: 35.15$

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			:DNA; 1295 BP.	INC. 50.85% 35.15% 26.42%		INC. 50.85\$ 35.15\$ 26.42\$		do 40 40		מנה מנה מנה	#168.	cotide #168. leotide #168. INC. 50.85\$ 35.15\$ 26.42\$	cDNA; 1295 BP. smembrane prote
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3 7 E		PD 01- PA (GE Percent Best Loc Query Ma	ID ADB15375 DE Human PR PN US200308	PD 08- PA (GE Percent Best Loc Query Ma	KESULT 924  ID ADB38627  DE Novel hur PN US200308	PA (GETH) Percent Simi Best Local S Query Match:	ID ADB	PD 08- PA (GE Percent Best Loc Query Ma	ID ADB665 DE Novel	PD 01-MAY-2 PA (GETH ) Percent Simil Best Local Si Query Match: RESULT 927	ID ADB8962 DE Human P. PN US20030 PA (GETH) PA (GETH) Percent Simi Best Local S Querry Match:	D ADB9035 DE Human P DN US20030 PN US20030 PA (CETH) PA (CETH) Percent Simi Best Local S Querry March:	ID ADE DE Hum

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60 standard; cDNA; 1295 BP.
human secreted and transmembrane protein PRO245 cDNA.
082764-A1.
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human secreted and transmembrane protein PRO245 cDNA.
082687-A1.
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secreted/transmembrane protein cDNA, #13.
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PRO polynucleotide SEQ ID NO 335.
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PRO polynucleotide SEQ ID NO 335.
077716-A1.
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PRO polynucleotide #168.
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H ) GENENTECH INC.

imilarity: 50.85$

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Single Si	USZU03073079-A1.  17-APR-2003. (GFTH) GENENTECH INC. rcent Similarity: 50.85% ref Local Similarity: 35.15% sry Match: 26.42% SULT 952 ADC50376 standard; cDNA,	Novel human secreted and trans US2003092106-Al. 15-MAY-2003. (GETH ) GENENTECH INC. rcent Similarity: 50.85\$ st Local Similarity: 35.15\$ sty Match: 26.42\$	ID ADC71923 standard; CDNA; 1295 BP. DB Novel human secreted and transmembrane protein PN USA003092107-A1. PD 15-MAY-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 50.85% Conservative:
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PA (GETH) GENEWIECH INC.  Percent Similarity: 50.85% Conservative Best Local Similarity: 26.42% Indels: RESULT 336  ID ADB35004 standard; CDNA; 1295 BP. DE Human PRO Polymuclectide SEQ ID NO 335. PP 24-APR-2003.  PA (GETH) GENEWIECH INC. Conservative Best Local Similarity: 50.85% Mismatches: Query March: 26.42% Indels: RESULT 399  PA (GETH) GENEWIECH INC. Conservative Best Local Similarity: 50.85% Mismatches: Conservative Best Local Similarity: 50.85% Mismatches: Query March: 26.42% Indels: Indels: Conservative Best Local Similarity: 50.85% Mismatches: Query March: 26.42% Indels: DE Human Recorded and transmembrane protein PN US-2003077720-A1. PA (GETH) GENEWIECH INC. Conservative Best Local Similarity: 50.85% Mismatches: Query March: 26.42% Indels: Indels: DE Novel human secreted and transmembrane protein PN US-200308269-A1. PP (GETH) GENEWIECH INC. Conservative Best Local Similarity: 50.85% Mismatches: Query Match: 50.85% Mismatches: DE Human secreted/transmembrane protein CDNA, #13 PP (GETH) GENEWIECH INC. Conservative Best Local Similarity: 50.85% Mismatches: RESULT 941  ID ADC33071 Standard; CDNA; 1295 BP. DE Human secreted/transmembrane protein CDNA, #13 PP CONSERVICT AND CONSERVATIVE Best Local Similarity: 26.42% Mismatches: RESULT 941  ID ADC33071 Standard; CDNA; 1295 BP. CONSERVATIVE Best Local Similarity: 26.42% Mismatches: RESULT 941  ID ADC33071 Standard; CDNA; 1295 BP. DE Human secreted/transmembrane protein CDNA, #13 PP CONSERVATIVE Best Local Similarity: 26.42% Mismatches: RESULT 943  ID ADC33071 Standard; CDNA; 1295 BP. DE Human secreted/transmembrane Protein CDNA, #13 PP CONSERVATIVE Best Local Similarity: 26.42% Mismatches: RESULT 943  ID ADC3907050720-941  PP CONSERVATION SECRETED SERVICT 943  ID ADC3907050720-941  PD CONSERVATION SECRETED SERVICT 943  ID ADC39070707007007007007007007007007007007007	φ ω	913 standard; cDNA; 1295 BP. secreted/transmembrane prote 3036061-A1. B-2003. ) GENENTECH INC. ) GENENTECH; 36.85\$ Similarity: 35.15\$ h:	RESULT 945  ID ADC34209 standard; cDNA; 1295 BP.  ID Human secreted/transmembrane protein cDNA, PN US2003036094-Al.  PD 20-FEB-2003.  PA (GETH ) GENENTECH INC.

Query Match: RESULT 962 ID APC59038 standar		rcent Simi st Local S ery Match:	ID AUC55916 standar DE Novel human secs PN US2003087360-A1. PD 08-MAY-2003.	S to the light	ID ADC58486 standar DE Novel human secr PN US2003087346-A1. PD 08-MAY-2003.	cent Simil t Local Si iry Match:	DE Human secreted/t PN US2003082541-A1. PD 01-MAY-2003.	9 7 7 E	ADDUSI6 Novel hi US20030 15-MAY-	Siry St	D ADCOULD'S STANDARD DE NOVEL human DE NOVEL human PN US2003087348-A1. PD 08-MAY-2003. PA (GFTH ) GENENTEC Percent Similarity: Best Local Similarity.	Query Match: RESULT 968 ID ADC69511 standar DE CDNA encoding hu PN US2003194770-A1.	rce st sry	DE Human PRO polynum DE Human PRO polynum PN US2003194773-A1. PD 16-OCT-2003. PA (GETH ) GENENTEC Percent Similarity: Best Local Similarity Query Match:
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Best Local Similarity: Query Match: RESULT 954	ID ADC59902 standard; cl DE Novel human secreted PN W2203092105-A1.	GOS: GENENTECH arity: milarity:	ADC52909 standard; Novel human secrete US2003087365-A1.	GENENTECH : arity: milarity:	RESULT 956 ID ADC57263 standard; cDNA; DE Novel human secreted and PN US2003087366-A1. PD 08-MNY-2003			-2003. ) GENENTECH : ilarity: Similarity:	KESULI 958 ID ADC50929 standard; CDNA; DE Novel human secreted and PN US2003087361-A1.	-2003. ) GENENTECH : ilarity: Similarity:	6 standard; RO polynucle 87362-Al. 2003. GENENTECH I	d,	PN US2003087363-A1. PD 08-MAY-2003. PD 06-MAY-2003. Percent Similarity: Best Local Similarity:	standard uman secre 87364-Al. 2003. GENENTECH larity: imilarity:

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Σ,	andard; secret 9-A1.	3-MAY-2003. BETH ) GENENTECH: Similarity: ccal Similarity:	KESULT 963 ID ADC55916 standard; DE Novel human secrete PN US2003087360-A1.	3-MAY-2003. BETH ) GENENTECH: Similarity: cal Similarity:	186 standard, human secret 1087346-A1.	PA (GETH ) GENENTECH ) Percent Similarity: Best Local Similarity:	KESOLI 963 ID ADC12307 standard; cDNA; 1295 DB Human secreted/transmembrane PN US2003082541-A1.		ADD03160 standard; cDNA; Novel human secreted and US2003092104-A1.	15-MAY-2003. (GETH ) GENENTECH ent Similarity: Local Similarity: / Match:	CG0152 standard; vel human secret 2003087348-Al.	08-MAY-2003. (GETH ) GENENTECH ent Similarity: Local Similarity: / Match:	0C69571 stand NA encoding 32003194770-P	(GETH ) GENENTECH ent Similarity: Local Similarity: // Match:	LT 969 LT 969 LT 960 standard; Human PRO polynucl US2003194773-A1. 16-OCT-2003. (GETH ) GENENTECH ent Similarity: Local Similarity: // Match:
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2203087354-Al.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003087358-Al.
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US2003104469-A1.
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RESULT 970

ID ADD09989 standard; CDNA; 1295 BP.

B Human PRO polynucleotide #168.

PN 16-0CT-2003.

PD 16-0CT-2003.

PA (GETH ) GENENTECH INC.

PA (ACTH ) GENENTECH INC.

PA (ACTH ) GENENTECH INC.

PRECENT SIMILARITY: 50.85%

Best Local Similarity: 35.15%

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US200319471-A1.
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Human PRO polynucleotide #168.
US2003194775-A1.
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PA (GETH) GENENTECH INC.

Percent Similarity: 50.6

Best Local Similarity: 35.1
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Percent Similarity: 50.
Best Local Similarity: 35.
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PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 50.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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PA (GETH ) GENENTECH
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RESULT 977
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ADD41150 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2003203438-Al.
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         ADD03868 standard; cDNA; 1295 BP.
Human secreted/transmembrane protein cDNA, #13.
US2003104381-A1.
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US2003194769-A1.
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cDNA encoding human PRO polypeptide #168.
US2003194792-A1.
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US2003194779-A1.
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US2003203431-A1.
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Percent Similarity: 50.85%
Best Local Similarity: 35.15%
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PA (GETH) GENENTECH INC.

Percent Similarity: 50.

Best Local Similarity: 35.
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Percent Similarity: 50.
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(eotide #168. INC. 50.85\$ 26.42\$	cDNA; 1295 BP. ed and transmemlINC.	50.85% 35.15% 26.42%	cDNA; 1295 BP. eotide #168.		.295 BP.	INC. 50.85% 35.15% 26.42%	: cDNA; 1295 BP. leotide #168.	INC. 50.85% 35.15% 26.42%	A; nd	INC. 50.85% 35.15% 26.42%	cDNA; 1295 BP. n PRO polypeptide	INC. 50.85\$ 35.15\$ 26.42\$	cDNA; 1295 BP. n PRO polypeptide		cDNA; 1295 BP. eotide #168.
DE Human PRO polynucleotide PN US2003203430-A1. PD 30-OCT-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 50.85 Best Local Similarity: 35.157 Query Match:	RESULT 987  ID ADD54152 standard, cDNA; 1  DE Novel human secreted and t PN US2003203432-A1.  PD 30-OCT-2003.  PA (GETH ) GENENTECH INC.	Percent Similarity: Best Local Similarity: Query Match:	DE Human PRO polynucleotide # DE US2001199030-A1.	2 2 2 2 3	RESULI 989 ID ADD91365 standard; CDNA; 1 DE Human PRO polynucleotide # PN US2003199055-A1. PD 23-OCT-2003.	2 4 4 4	AESOLI 230 ID ADE03979 standard; DE Human PRO polynucl PN US2003199057-Al.	PD 23-OCT-2003. PA (GETH ) GENENTECH IN Percent Similarity: 9 Best Local Similarity: 2 Query Match:	RESULT 991 ID ADE32276 standard; cDN DE Novel human secreted a PN US2003194765-A1.	PD 16-OCT-2003. PA (GETH) GENENTECH : Percent Similarity: Best Local Similarity: Query Match:	ID ADE22208 standard; cDNA; DE CDNA encoding human PRO pr 022003199056-A1.	GENENTECH arity: milarity:	ADD79432 standard; cDNA; 1 DE cDNA encoding human PRO po PN US2003203428-Al.	PA (GETH) GENENTECH I Percent Similarity: Best Local Similarity:	KESULI 994 ID ADE41968 standard; cDNA; DE Human PRO polynucleotide

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Query Match:
RESULT 998

ID ADE33932 standard, cDNA, 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003194791-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003194767-A1.
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Human secreted/transmembrane protein cDNA, #13
US2003077583-A1.
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cDNA encoding human PRO polypeptide #168.
US2003207417-A1.
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DE ADB19441 standard; CDNA; 1295 BP.

DE Human PRO polynucleotide #168.

PN US2003199025-A1.

PD 23-CCT-2003.

PA (GETH) GENENTECH INC.

Percent Similarity: 50.85*

Query Match: 26.42*
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                                                                                 Human PRO polynucleotide #168. US2001199023-A1.
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Human PRO polynucleotide #168.
US2003199053.Al.
23-OCT-2003.
(GETH ) GENENTECH INC.
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PN US200194791-A1.

PN US201194791-A1.

PD 16-OCT-2003.

PA (GETH ) GENENTECH INC.

Percent Similarity: 50.85$

Best Local Similarity: 35.15$

"""EY Match: 26.42$

"""EY Match: 26.42$

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                                                                                                                                                                                                                                                                                                                                     Query Match:
RESULT 997
ID ADE3380 standard; cDNA; 1295
DE Novel human secreted and tran
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENEVTECH INC.
Percent Similarity: 50.85%
Best Local Similarity: 35.15%
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DE CDNA encoding human PRO poly
PN US200320417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 50.85%
Best Local Similarity: 35.15%
QUETY Match:
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DE Human PRO polynucleotide #16
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 50.85%
Best Local Similarity: 35.15%
Query Match:
RESULT 1001
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PD 23-OCT-ZOGO.

PARTH J GENTH INC.

Percent Similarity: 50.85%

Best Local Similarity: 35.15%

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Best Local Similarity: 35.15%
Query Match: 26.42%
PD 16-OCT-2003.

PA (GETH ) GENENTECH INC.

Percent Similarity: 50.

Best Local Similarity: 35.
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RESULT 995
ID ADB17785
DE Human PRO
PN USC03199
PD 23-OCT-20
PA (GETH ) G
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RESULT 996
ID ADD919
DE Human
PN US2003
PD 23-OCT
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2003. GENENTECH larity: imilarity:	standard; O polynucle 9026-Al. 003. GENENTECH I arity: milarity:	RESULT 1004  1D ADE43085 standard; CDNA, DE Human PRO polynucleotide PN US2003199033-A1. PD 23-OCT-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 50.854 BGEL Local Similarity: 35.154 QUETY MACCH: 26.424 RESULT 1005 1D ADD5874 standard; CDNA, DE Human PRO polynucleotide PN US2003199059-A1.	PA C3-0CT+ 2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 50.86  Best Local Similarity: 35.15  Query Match: 26.43  RESULT 1006.  ID ADE22760 standard; cDNA,  DE CDNA, encoding human PRO US2003199064-A1.	3. INENTECH :ity: :larity:	standard; oding humar 3429-Al. 003. GENENTECH l arity: milarity:	standard, an secret 766-Al. 33. SNENTECH rity: Llarity:	RESULT 1009  DE ADE42520 standard; CDNA; 1295 BP.  DE Human PRO polynuclectide #168.  N US203199032-A1.  PD 23-OCT-2003.  PA (GETH ) GENEWRECH INC.  Percent Similarity: 50.85\$ Mismat.  Best Local Similarity: 35.15\$ Mismat.  CONSER RESULT 1010  ID ADD80536 standard; CDNA; 1295 BP.  DE CDNA encocing human PRO polypeptide #168  PD 06-NOV-2003.
PD PA Perce Best Query	DE DE PN PD PC PEC PEC PEC PEC PEC PEC PEC PEC PEC	RESU ID DE PN PO PEC BEST QUEL RESU ID DE	PD PA Perc Best Quer RESU ID DE	PD PA Perc Best Quer	DE D	KESU ID DE PN PD PA Pero	RESU 110 110 PN PD PA RESU ID PN PN

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ADG21485 standard; cDNA; 1295 BP. Novel human secreted and transmembrane protein PRO245 cDNA. US2003207355-A1.
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NADG23126 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207384-A1.
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RESULT 1018

ID ADG80525 standard; CDNA; 1295 BP.

DE Human PRO polynucleotide #168.

PD US2003207373-A1.

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SULT 1014
ADE92776 standard; CDNA; 1295 BP.
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Human PRO polynucleotide #168.
US2003207370-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity; 50.85
Best Local Similarity; 35.15$
Query Match:
RESULT 1011
ID ADD89564 standard; cDNA; 1295 BP
DE Human PRO polymucleotide #168.
PN US2003199028-A1.
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PN US2003199031-A1.

PA (GETH ) GENENTECH INC.

Percent Similarity: 50.88$

Best Local Similarity: 35.15$

QUERY MACCH:

TRESULT 1013

ID ADE04647 standard; CDNA; 1295 BP

DE Human PRO polynucleotide #168.
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US2003194777-A1.
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PA (GETH ) GENENTECH INC.
Percent Similarity: 50.85%
Best Local Similarity: 35.15%
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PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 50.85%
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PA (GETH) GENENTECH INC.
Percent Similarity: 50.85%
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PA (GETH) GENENTECH INC.

Percent Similarity: 50.85%

Best Local Similarity: 35.15%

Query Match: 26.42%

RESULT 1017
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Percent Similarity: 50.85
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Query Match: 26.42
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ADE40848 standard;
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Percent Similarity: Best Local Similarity: Query Match:	RESULT 1019 ID ADG79973 standard; CDNA; DE Human PRO polynucleotide PN US2003207372-A1. PD 06-NOV-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 50.85' Best Local Similarity: 35.15' Query Match: 26.42'	1D ADH62535 standard; of the bound of the bo	Percent Similarity: Best Local Similarity: Query Match:	DE Human secreted/trailing US2003039972-A1.	FU Z/-FEB-2003. PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Ouery Match:	TESOLI 1022 1D ADH55265 standard; CDNA; 1 DE Novel human secreted and t PN US2003207381-A1.	PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Query Match: RESULT 1023	1D ADH55817 standard; cDNA; 1D Novel human secreted and the US2003207379-A1.	PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match: RESHIT 1024	ID ADI37958 standard; cDNA; 1295 Bi DE Human secreted/transmembrane pro PD 20-MAR-2003.	PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match:		SENENTECH arity: nilarity:

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Y Match: 26.42% Indels: 16
ILT 1031
ACD24020 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA. US2003032156-A1.
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ADHB1346 standard, CDNA, 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
1922032073777-Al.
06-NOV-2003.
ADI64985 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 CDNA.
US2003207386-Al.
                                                                                                                                                      Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207387-A1.
06-NOV-2003.
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Novel human secreted and transmembrane protein PRO245 cDNA.
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TAT 1031

TAT 1031

CDNA, 1295 BP.

CDNA encoding human PRO polypeptide #168.
US2003004311-A1.
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Tur 1032
ACAS8345 standard; CDNA, 1295 BP.
CDNA encoding human PRO polypeptide #11.
19-DEC-2002.
(GETH ) GENENTECH INC.
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20.3c.

20.3c.

3CULT 1030

D ACAS8948 standard; cDNA; 1295 BP

E Human PRO polynucleotide #11.

PD 10-OCT-2002.

PA (EETH) GENENTECH INC.

Percent Similarity: 50.85%

Best Local Similarity: 25.15%
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LT 1034
ADJ26226 standard; cDNA; 1295 BP
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(GETH) GENENTECH INC.
rcent Similarity: 50.85%
st Local Similarity: 35.15%
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(GETH ) GENENTECH INC.

rcent Similarity: 50.85%

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(GETH) GENERIECH INC.
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(GETH) GENENTECH INC.
Ent Similarity: 50.85%
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II 1028
ADH81898 standard;
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ADI63484 standard;
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us-10-785-220b-1.p2n.rng.spdi

PN US2003100087-A1.  PD 29-MAY-2003.  PA (GETH) GENENTECH INC.  Percent Similarity: 50.85\$ Conservative: 46  Best Local Similarity: 35.15\$ Mismatches: 128  Query Match: 26.42\$ Indels: 16  RESULT 1043  ID ADDRAS84 standard; cDNA; 1295 BP.  DE Human PRO polynucleotide #168.	2 2 2 2	g # # g	numin Seriecu/Lianshemulane process constant (22003130489-A1.  10-JUL-2003.  (GETH ) GENENTECH INC.  (GETH ) Similarity: 50.85\$ Mismatches: str. Match: 26.42\$ Indels: STT. 1046  ADB75756 standard; CDNA; 1295 BP. Human PRO Polymucleotide #168.	Al.  TECH INC.  50.85\$  Conservative:  ity: 35.15\$  Mismatches:  26.42\$  Indels:  dard, cDNA, 1295 BP.  4/Lransmembrane protein cDNA, #13.  HI.	50.85\$ CONSELVATIVE: 35.15\$ Mismatches: 26.42\$ Indels: 1; cDNA; 1295 BP. nan PRO polypeptide #168.	Percent Similarity: 50.85% Conservative: 46 Best Local Similarity: 35.15% Mismatches: 128 Query Match: 26.42% Indels: 16 RESULT 1049 ID ADE23864 standard; cDNA; 1295 BP. DE CDNA encoding human PRO polypeptide #168. PN US2003092110-A1.	st st sury sury
Human secreted/transmembrane protein cDNA, #13. US2003054449-A1. 20-MAR-2003. (GETH) GENENTECH INC. (GETH) GENENTECH INC. S0.85* Conservative: 46 st Local Similarity: 35.15* Mismatches: 128 sry Macch: 26.42* Indels: 16 SULT 1035 ADM82515 standard; cDNA, 1295 BP.	DE Novel human secreted and transmembrane protein PRO245 cDNA.  PN 08-MAY-2003. PD 08-MAY-2003. PA (GETH ) GENENTECH INC. PERCENT Similarity: 50.85\$ Conservative: 46 Best Local Similarity: 35.15\$ Mismatches: 128 Query Match: 26.42\$ Indels: 16 RESULT 1036 ID ADNI5914 standard; cDNA; 1295 BP. DE Novel human secreted and transmembrane protein PRO245 cDNA.	US2003087353-A1.  08-MAY-2003. (GETH ) GENENTECH INC. (GETH ) SENSTECH INC. Cort Similarity: 50.85% Conservative: 46  st Local Similarity: 35.15% Mismatches: 128  rry Match: 26.42% Indels: 16  SULT 1037 standard: CDNA. 1295 RP	dr to	Novel human secreted and trans US2003087356-A1. 08-MAY-2003. (GETH ) GENENTECH INC. rcent Similarity: 50.85\$ st Local Similarity: 35.15\$ sty Match: 26.42\$ SULT 1039 ADN14810 standard; cDNA; 1295 Novel human secreted and trans US2003087357-A1.	(GETH ) GENENTECH (GETH ) GENENTECH st Local Similarity: sry Match: suLr 1040 NOV21 Numan secret US2003092115-A1. 15-MAY-2003.	PA (GETH) GENENTECH INC.  Percent Similarity: 50.85\$ Conservative: 46  Best Local Similarity: 35.15\$ Mismatches: 128  Query Match: 26.42\$ Indels: 16  RESULT 1041  ID ADE79141 standard; CDNA; 1295 BP.  DB Human secreted/transmembrane protein CDNA, #13.	rce sty SUL

46 128 16	46 128 16	46 128 16	46 128 16	46 128 16	46 128 16	46 128 16	46 128 16
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4C. 50.85% 35.15% 26.42%	otide #168. 7C. 85.158	BP.	) )	cDNA, 1295 BP. ectide #168. INC. 50.85\$ 35.15\$ 26.42\$	cDNA, 1295 BP. ectide #168. INC. 50.85\$ 35.15\$ 26.42\$	BP. rot	cDNA; 1295 BP.  nn PRO polypeptide  INC. 35.085\$ 26.42\$  cDNA; 1295 BP.  cDNA; 1295 BP.
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PA (GETH ) GENENTECH INC Percent Similarity: 50 Best Local Similarity: 35 Query March: 26 RESULT 1059 ID ARBS2218 standard; CD COMA encoding human Pi	PN USZUGJAJADUSZALI. PD 23-OCT-2003. PA (GETH) GENENTECH INC. Percent Similarity: 50.85% Best Local Similarity: 35.15% QUETY Match: 26.42% RESULT 1060 ID ADE93328 standard; cDNA; 1 DE Human PRO polynucleotide † PN USZUGJ199060-A1.	PA (GETH ) GENENTECH INC Percent Similarity: 35 Query Match: Senilarity: 35 Query Match: Cod. Similarity: 56 CODE CODE SIMILARITY: 57 CODE CODE SIMILARITY: 57 CODE CODE SIMILARITY: 57 CODE CODE CODE STANDARD PROJECT CODE CODE CODE CODE CODE CODE CODE CODE	PA (GETH ) GENENTECH INC.  Percent Similarity: 50.85\$ Conse Best Local Similarity: 35.15\$ Misma Query Match: 26.42\$ Indel  RESULT 1062  ID ADE98449 standard; CDNA; 1295 BP.  DE Human secreted/transmembrane protein CE PD 13.NOV-2003.	PA (GETH ) GENENTECH INC. Percent Similarity: 50.85% Best Local Similarity: 35.15% Query Match: 26.42% RESULT 1063 ID ADB92224 standard; cDNA; DE Novel human secreted and	PD 23-OCT-2003. PD 23-OCT-2003. Percent Similarity: Best Local Similarity: Buery Match: RESULT 1064 ID ADE90525 standard; DE Human PRO polynucle PN US2003199063-A1. PD 23-OCT-2003.	PA (GETH ) GENENTECH Percent Similarity: Percent Similarity: Query Match: RESULT 1065 ID ADE91672 standard; DE Novel human secret PN US2003199058-A1.	PA (GETH) GENERATECH INC. Percent Similarity: 50.85\$ Percent Similarity: 50.85\$ Query Match: 26.42\$ RESULT 1066 ID ADB98976 standard; cDNA; 1295 DB Human secreted/transmembrane pp PP US2003211568-A1. Pp 13-NOV-2003.
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rcent Similarity: st Local Similarity ery Match: SULT 1067 ADG40346 standar: Human secreted/t. US200325253-A1. 04-DEC-2003. (DESN/) DESNOYER. (GODD/) GODDARD (GODD/) GODDARD (GODD/) GODWSKI (GUBN/) GURNYY A	7.5. 2.9.	PA (GETH) GENERTECH INC. PA (GETH) GENERTECH INC. Percent Similarity: 50.85% Best Local Similarity: 35.15% Query Match: 26.42% RESULT 1069 D ADGO2251 standard; CDNA; 1295 BP DE Human PRO polynucleotide #168.	US2003207352-A1. 06-NOV-2003. (GETH ) GENENTECH INC. cent Similarity: 50.85; ry Match: 51.15; ULT 1070 NOVEL ) Novel human secreted and	INC. 50.85% 35.15% 26.42% CDNA;	PN US2003207376-A1.  PD 06-NOV-2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 50.85\$ CC  Best Local Similarity: 35.15\$ Mi  Query Match: 26.42\$ Ir  RESULT 1072  ID ADF98013 standard; CDNA; 1295 BP.  DB Human PRO Polynucleotide #168.	2 t	PN US2003207426-A1. PD 06-NOV-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 50.85\$ Best Local Similarity: 35.15\$ Query Match: 26.42\$ RESULT 1074

US2003207356-A1.

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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207424-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207427-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
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Novel human secreted and transmembrane protein PRO245 cDNA.
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Novel human secreted and transmembrane protein PRO245
US2003207389-A1.
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ADG15511 standard, cDNA, 1295 BP.
cDNA encoding human PRO polypeptide #168.
US2003219885-A1.
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RESULT 1084
ID ADF96909 standard; CDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207371-A1.
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US2003207374-A1.
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US2003207423-A1.
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PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 50.85 Best Local Similarity: 35.15 Query Match: 26.42 RESULT 1083
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ID ADG06094 standard,
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ADG56868 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207364-A1.
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207365-A1.
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US2003207362-A1.
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Novel human secreted and transmembrane protein PRO245 CDNA,
US2003207390-Al.
                                                                              AUGS5212 standard; cDNA; 1295 BP.
Novel human secreted and transmembrane protein PRO245
US2003194778-A1.
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Human PRO polynucleotide #168.
US2003207358-A1.
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PD 06-NOV-2003.  PA (GETH ) GENEWTECH : Percent Similarity: Best Local Similarity: Query Match:	ACCOUNT ADGESS24 standard; cDNA; DE Novel human secreted and PN US2003207368-A1. PD 06-NOV-2003.	(GETH ) GENENTECH cent Similarity: st Local Similarity:	ID ADG70890 standard, CDNA; DE Novel human secreted and	2003. GENENTECH Jarity: imilarity:	JULT 1101 ADG92586 standard Human secreted/tra	3 # Z	RESULT 1102 ID ADG57972 standard; cDNA; DE Novel human secreted and PN US2003207363-A1.	06-NOV-2003. (GETH) GENENTECH ccent Similarity: tt Local Similarity: xry_Match:	RESULT 1103 ID ADG53556 standard; CDNA; DE Novel human secreted and PN US200320/415-A1.	(GETH ) GENENTECH cent Similarity: t Local Similarity: rry Match:	KESULI 1104  ID ADG71442 standard; DE Novel human secrete PN US2003207421-A1.	(GETH ) GENENTECH (GETH ) GENENTECH cent Similarity: of Local Similarity: sty Match:	ID ADGB1629 standard; DE Human PRO polynucle PN US2003207805-A1. PD 06-NOV-2003. Percent Similarity: Best Local Similarity: Query Match:	KESULT 1106  ID ADH30591 standard, CDNA, DB Human PRO polymucleotide PN US2003077723-A1. PD 24-APR-2003. PA (GETH ) GENENTECH INC.

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Percent Similarity: Best Local Similarity: Query Match: RESULT 1107 RESULT 1107 RESULT 1107 DE Novel human secrete PN US2003207419-A1. PD 06-NOV-2003. PA (GETH) GENEWIECH 1 Percent Similarity: Best Local Similarity: DESULT 1108	ID ADG52380 standard; CDNA; 1D Novel human secreted and the US2003207414-A1.  PD 06-NOV-2003.  PA (GETH) GENENTECH INC.  Percent Similarity; 50.85% Best Local Similarity; 35.15% Query Match: 26.42% RESULT 1109  ID ADG54108 standard; CDNA; 1DE Novel human secreted and the Novel	Sear Sear	standard, an secret 366-A1. 303. ENSTECH rity: 1larity: 1larity: 318-A1.	PA (GETH) GENENTECH INC. PA (GETH) GENENTECH INC. Percent Similarity: 50.85% Best Local Similarity: 35.15% Query Match: 26.42% RESULT 1113 ID ADG61428 standard; CDNA; DE Novel human secreted and PN US2003207429-A1. PA (GETH) GENENTECH INC. Percent Similarity: 35.15% Best Local Similarity: 35.15%	Query Match: Cuery Match: D ADH28515 standard; cDNA; DE Human PRO polynucleotide PN US2003022331-A1. PD 30-JAN-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 50.85%

PA (GETH ) GENI Percent Similarit	Query Match: RESULT 1122 ID AD118545 Btr	DE HUMAN SECTED PN US2003152999 PD 14-AUG-2003 PA (GETH ) GENI Percent Similarit	Best Local Simila Query Match: RESULT 1123 ID AD165265 Sto		Best Local Simila Query Match: RESULT 1124	gr, tre	DE Novel human DE Novel human PN US200400546 PD 15-JAN-2004 PA (GETH) GENH Percent Similarit Best Local Simila RESHLT 1126	.,	PA (GETH ) GENT Percent Similaril Best Local Simila Guery Match: RESULT 1127 ID AD11538 8tc	PN US2003207385 PD 06-NOV-2003 PA (GETH ) GENI Percent Similarit Best Local Simila	TO ADGOSLS SEE  TO ADGOSLS SEE  DE Novel human  PN US200400954'  PD 15-JAN-2004  PA (GETH ) GENI  PATE (CAST SIMILARY)	Ouery Match: RESULT 1129 ID AD165692 Stc DE Human secret PN US2001148371 PD 07-AUG-2003
128 16	RO245 CDNA.	46 128 16	RO245 CDNA.	46 128 16	46 198	16		46 128 16	46 128	16	v.	128 16
Mismatches: Indels:	1295 BP. transmembrane protein PRO245	Conservative: Mismatches: Indels:	1295 BP. transmembrane protein PRO245	Conservative: Mismatches: Indels:	rane protein cDNA, #13.  Conservative:	#		Conservative: Mismatches: Indels:	1295 BP. rane protein cDNA, #13. Conservative:	Indels: .295 BP. ine protein cDNA, #13.	25.7	Mismatches: Indels: 1.295 BP.
Similarity: 35.15%	60 standard; cDNA; human secreted and 207367-A1.	PD 00-NOV-2003.  Percent Similarity: 50.85% Best Local Similarity: 35.15% Query Match: 26.42%	standard; cDNA; man secreted and	PD 05-NOV-2003.  PRA (GETH ) GENENTECH INC.  PRACENT Similarity: 50.85%  Best Local Similarity: 35.15%  Query Match: 26.42%	standard; cDNA; creted/transmemb) 5533-A1. 004. GENENTECH INC. arity: 50.855	standard; creted/trar 6211-A1	08-JAN-2004. (DESN/) DESNOYERS I. (GODD/) GODDARD A. (GURN/) GURNEX P J. (MATH/) MYTHER J P. (WILL/) WILLIAMS P M. (WOODN/) WOOD W I.	Percent Similarity: 50.85% Best Local Similarity: 35.15% Ouery Match: 26.42% RESULT 1119	standard; cDNA; creted/transmemb 5904-Al. 003. GENENTECH INC. arity: 50.85; milarity: 35.155	standard; creted/tran 5665-Al. 004.	4 · ખે પાં ખું ખ	Local Similarity: 35.15% Wismant Local Similarity: 35.15% Mismatch: 26.42% Indels T 1121 T 1121 Standard; CDNA; 1295 BP. CDNA encoding human PRO polypeptide #168 US2003207361-A1.
Best Local S Query Match:	ABSOLITITE TD ADG54660 St. DE Novel human PN US200320736	PA (GETH) GENEUT PACCENT SIMILIARITY BEST LOCAL SIMILARITY Query Match:	RESULT 1116 ID ADG59700 DE NOVEL hu PN US200320	PD 06-NOV-2003. PA (GETH ) GENENT) Percent Similarity; Best Local Similarity Query Match:	RESULT 1117  DADH20375 stand, DE Human secreted, PN US200405553-A, PD 08-JAN-2004. PA (GETH ) GENENT; PREFCENT SIMILarity;	ŽĮ.	PA (BESN/) PA (GODD/) PA (GODD/) PA (GODO/) PA (GURN/) PA (MATH/) PA (WILL/) PA (WOOD/)	Percent Similarity: Best Local Similari Query Match: RESULT 1119	ID ADH59775 stand, DE Human secreted, PN US2003215904-A, PD 20-NOV-2003. PA (GETH) GENENT; Percent Similarity: Best Local Similarity:	ŗij	PA (GODO/) PA (GODO/) PA (GURN/) PA (MATH/) PA (WOLD/) PA (WOOD)	Destruction Similarity: Cuery Match: RESULT 1121 ID AD181124 standard DE CDNA encoding hum PN US2003207361-A1. PD 06-NOV-2003.

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tandard; cDNA; 1295 BP.
n secreted and transmembrane protein PRO245 cDNA.
47-A1.
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82-A1.
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71-A1.
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	PD 09-0CI-20 PA (GETH ) GI Percent Simila. Best Local Sim	Query Match:     RESULT 1138     ID AD77441 to     DE Human PRO     PN US2004038:	, Š	Query Match: RESULT 1139 ID ADJ65563 8	DE CDNA enco PN US2004038: PD 26-FEB-20 PA (GETH ) GI	cent Simi	Query Match: RESULT 1140	DE CDNA enco	PD II-MAK-200 PA (GETH ) GI		ζĘ	1D ADM42423 8 DE CDNA encoc PN US20040584 PD 25-MAR-200	PA (GETH ) GI Percent Similar	Query Match:	1D AD006098	DE AUMAII FRO PN US6686451- PD 03-FEB-200	Ş	Best Local Simi	Query Match: RESULT 1143		PD 15-APR-200 PA (GETH ) GE	r Ce	Query Match: RESULT 1144	ID ADM28285 E DE CDNA encoc PN US20040770 PD 22-APR-200	r G	Query Match: RESULT 1145
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46 128 16	PRO245 CDNA.	46 128 16					128 16	PRO245 cDNA.		46 128	16		46	128 16	) 1			46	128 16			46	128 16	PRO245 CDNA.		128 16
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Percent Similarity: Best Local Similarity: Query Match:	DE Novel human secreted and PN US2003207383-A1.	PD 06-NOV-2003.  PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Query Match:	UT 1131 ADH60435 standard; CDNA; 1295 BP. Human secreted/transmembrane protein INSO004003311-11	05-FEB-2004. (DESN/) DESNOYERS (GODD/) GODDARD A.		(WOOD/) WOOD W I.	Best Local Similarity: Query Match:	ID ADI18265 standard; cDNA; DE Novel human secreted and	0SZ003Z0/349-A1. 06-NOV-2003. (GETH ) GENENTECH		Query Match:	ADJ9942 standard; cDNA; 1295 BP. Human secreted/transmembrane protein cDNA, US2001187238-A1.	02-OCT-2003. (GETH ) GENENTECH ant Similarity:	imilarity:	RESULT 1134	Augustia Berreteald, Cons, 1233 Br. Human secreted/transmembrane protein CDNA, US2003186358-A1.	02-OCT-2003.	Percent Similarity:	••	ADM25030 standard; Human secreted/tra		<b>T</b> :	Best Local Similarity: Query Match:	of 1136 ADJ63546 standard; cDNA; Novel human secreted and US2004039164-A1.	3-2004. ) GENENTECH nilarity:	Best Local Similarity: Query Match: RESHT, 1137
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ein cDNA, #13.	Conservative: Mismatches: Indels:		Conservative: Mismatches: Indels:	de #168.	Conservative: Mismatches: Indels:	de #168.	Conservative: Mismatches: Indels:	ide #168.	Conservative: Mismatches: Indels:	Conservative: Mismatches: Indels:	Conservative:	smatches idels: #168.	Conservative: Mismatches: Indels:
6 standard; cDNA; 1295 BP. ecreted/transmembrane protein 90611-A1.	INC. 50.85\$ 35.15\$ 26.42\$	υO	INC. 50.85% 35.15% 26.42%	DNA; 1295 BP. PRO polypepti	INC. 50.85% 35.15% 26.42%	cDNA; 1295 BP. n PRO polypepti	INC. 50.85\$ 35.15\$ 26.42\$	NA; 1295 BP PRO polypept	INC. 50.85 <b>\$</b> 35.15 <b>\$</b> 26.42 <b>\$</b>	cotide #13. eotide #13. INC. 50.85% 26.42%	. 85	35.15* Mi 26.42\$ Ir cDNA; 1295 BP. n PRO polypeptide	00.03 W 4.14
ADM2977 Human 8 US20031	2 12 12 12	Jour 1138 ADJ7741 standard; Human PRO polynucl US2004038336-A1. 26-FEB-2004.	2 2 2 2 2	KESOLI 1139  ID ADJ65563 standard; C  DE CDNA encoding human PN US2004018335-A1.	04. ENENTECH rity: ilarity:	KESULI 1140 ID ADM27699 standard; cl DE CDNA encoding human i PN 1152004048131-A1	11-MAR-2004. (GETH ) GENENTECH Crent Similarity: st Local Similarity:	ADM42423 standard; cC cDNA encoding human F US2004058424-Al.	25-MAK-2004. (GETH) GENENTECH fcent Similarity: st Local Similarity: sty Match:	006098 standard; Man PRO polynucl 6686451-B1. -FEB-2004. ETH ) GENENTECH Similarity: cal similarity:	andard; 5 gene. 5-A2. ENTECH	st Local Similarity: ery March: SULT 1144 ADM28285 standard; cDNA.encoding huma	US2004077064-A1. 22-APR-2004. (GETH ) GENENTECH rcent Similarity: Bt Local Similarity: PAY Match: SULT 1145 ADR10950 standard;
DED	O B B B B B	SPEC	PA Pe		O B B B B		Oge Begge	2082 2082	PA P		P P P P P P P P P P P P P P P P P P P	8 9 8 G B	PP

Mismatches: Indels:

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Query Match:
RESULT 1154

RESULT 1154

DD AAFTA414 standard; DNA; 905 BP.
DE Anglogeneeis protein AAAl nucleotide sequence (Fig 7)

PN WO200111086-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX81770 standard; cDNA; 1295 BP.
cDNA DNA35638 encoding A33 related antigen PRO245.
WO9927098-A2.
                                                 ADS74498 standard; cDNA; 1295 BP.
Human secreted/transmembrane cDNA #13.
US2004185531-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
RESULT 1153
ID AA161103 standard; cDNA; 930 BP.
DE Human polynucleotide SEQ ID NO 5092.
PN WO200153312-A1.
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Query Match:
RESULT 1156
ID AAX56523 standard; DNA; 396 BP.
DE Human T84016 DNA fragment.
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RESULT 1155
ID AAX37717 standard, DNA; 297 BP.
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PA (EOSB-) EOS BIOTECHNOLOGY INC.
Percent Similarity: 56.11%
Best Local Similarity: 39.37%
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PD 03-JUN-1999.
PA (GETH ) GENENTECH INC.
Percent Similarity: 50.85%
Best Local Similarity: 35.15%
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Best Local Similarity: 38.50%
Query Match: 25.87%
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WILLIAMS P M.
WOOD W I.
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PA (GETH ) GENENTECH INC.

Percent Similarity: 81.

Best Local Similarity: 81.
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DESNOYERS L.
EATON D L.
FERRARA N.
FILVAROFF E.
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MATHER J P.
PAN J.
PAONI N F.
ROY M A.
STEWART T A.
                                                                                                                     ASHKENAZI A.
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HILLAN K J.
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Best Local Similarity:
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                                                                                                                                                                                                                   FONG S.
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                                                                                                   23-SEP-2004
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(WILL/)
(WOOD/)
                    Query Match:
RESULT 1151
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(DESN/)
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(MATH/)
(PANJ/)
(PAON/)
(ROYM/)
(STEW/)
                                                                                                                     (ASHK/)
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(FERR/)
(FILV/)
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Novel human secreted and transmembrane protein PRO245 cDNA.
US2003207354-Al.
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DE Human secreted/transmembrane protein cDNA, #13.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 50.85$ Conservative: 4
Best Local Similarity: 35.15$ Mismatches: 1
Query Match: 26.42$ Indels: 1
RESULT 1146
ID ADR17859 standard; cDNA, 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2004147017-A1.
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cDNA encoding human PRO polypeptide #168.
US2003077659-A1.
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ID ADT03535 standard; CDNA; 1295 BP.
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Human PRO245 cDNA sequence.
AU2003259607-A1.
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DE Human PRO245 cDNA sequence.
PN AU200225607-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 50.85$
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(GETH) GENENTECH INC.
nt Similarity: 50.85%
Local Similarity: 35.15%
Match: 26.42%
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26.42%
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PD 24-APR-2003.
PA (GETH ) GENENTECH INC. Percent Similarity: 50.85 Best Local Similarity: 35.15 Query Match: 26.42 RESULT 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID ADT0353s standard; cDNA;
DE Human secreted/cransment
PN USC03152922-A1.
PD 14-AUG-2003.
PA (GETH ) GENERTECH INC.
Percent Similarity: 35.15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAN J.
PAONI N F.
STEWART T A.
TUWAS D.
WILLIAMS P M.
                                                                                                                                                                                                                                                                                                                                   GERBER H.
GERRITSEN M E.
                                                                                                                                                                                                                                                                                                                                                                 GODDARD A.
GODOWSKI P J.
GRIMALDI C J.
                                                                                                                                                                                                                                                                                                                                                                                                                      GURNEY A L.
HILLAN K J.
KLJAVIN I J.
                                                                                                                                                                                                ASHKENAZI A.
BOTSTEIN D.
DESNOYERS L.
                                                                                                                               DE Human secreted/transi

DE Human secreted/transi

PA (ASHK/) ASHKENAZI A.

PA (ASHK/) ASHKENAZI A.

PA (BOTS/) BOTSTEIN D.

PA (BOTS/) BOTSTEIN D.

PA (EATO/) EATON D L.

PA (EATO/) FILVAROFF B.

PA (GAOW) GAO W.

PA (GERR)/ FERRARA N.

PA (GERR)/ FERRARE H.

PA (GERR)/ GERRITSEN M.

PA (GERR)/ GERRITSEN M.

PA (GEND)/ GODDREN P.

PA (GEND)/ GODDREN P.

PA (GEND)/ GODDREN P.

PA (GENN)/ GERMITSEN M.

PA (GINN)/ GENMEN A L.

PA (HILL)/ HILLAN J.

PA (HILL)/ HILLAN J.

PA (HILL)/ PANIN I J.

PA (RLJA)/ KLJAVIN I J.

PA (RLJA)/ KLJAVIN I J.

PA (RLJA)/ RLJAVIN I J.

PA (RLJA)/ RLJAVIN I J.

PA (RLJA)/ STEWAT T.

PA (WODD)/ WOOD W I.

PECCENT SIMILITANS P.

PA (WOOD)/ WOOD W I.
                                                                                                                                                                                                                                                                                     FILVAROFF E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MATHER J P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
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46 128 16

Conservative: Mismatches: Indels:

Conservative: Mismatches: Indels:

39 89 11

Conservative: Mismatches: Indels:

138

Conservative: Mismatches: Indels:

37 86 11

Conservative: Mismatches: Indels:

INC. Conservative: 14 Mismatches: 22 Indels: 2	INC. Conservative: 14  * Mismatches: 22  * Indels: 2 367 BP.	Conservative Mismatches: Indels:	rel protein SEQ ID NO 41.  INC. Conservative: 14  Mismatches: 22  Indels: 2  trickles: 14  indels: 14  intels: 17  intels: 17	Conservative: 0  Mismatches: 0  Indels: 0  1430 BP.	CC MM	Conservative: 0 Mismatches: 0 Indels: 0	Conservative: 0 Mismatches: 0 Indels: 0
WO200155320-A2. 02-AUG-2001. (HUMA-) HUMAN GENOME SCI recent Similarity: 79.65% st Local Similarity: 67.26% sry Match: 23.61% SULT 1165 ABA0658 standard; CDNA; HUMAN CDNA SEQ ID NO: 324	PN WOZOULS474.A2. PD 02-AUG-2001. PA (HUMA) HUMAN GENOME SCI IN Percent Similarity: 79.65% Guery Match: 23.61% RESULT 1166 ID ABN83995 standard; cDNA; 36 DE Human polymucleotide SEQ II	PD 11-JUL-2002. PA (ROSE/) ROSEN C A. PA (RUBE/) RUBEN S M. PA (BARA/) BARASH S C. Percent Similarity: 79.65% Best Local Similarity: 67.26% Query Match: 23.61% RESULT 1167 ID ADB31520 standard; cDNA; 367	Human cDNA encoding US2003077606-A1. 24-APR-2003. (HUMA-) HUMAN GENOICE Similarity: et Local Similarity: ery Match: ULT 1168 AAX56514 standard; Human 225257 DNA	NC. 100.00 100.00 23.454 cDNA;	W0200175067-A2.  H.OCT-2001.  (HYSE-) HYSEO INC.  Similarity: 34.649  St Local Similarity: 34.699  Sty Match: 23.159  SULT 1170  AAX56503 standard; DNA; ZHUMA: 31.2476	rce at sury sury	rce Sury
	48 137 18			48 138 19 ing sequence.	47 136 24 D4731.	3.6 11	14 22 2 SEQ ID NO: 2303.
Conservative: 0 Mismatches: 1. Indels: 9	Conservative: Mismatches: Indels:	Conservative: 0 Mismatches: 0 Indels: 0	Conservative: 0 Mismatches: 0 Indels: 0 P.	Conservative: Mismatches: Indels: .	Conservative: Mismatches: Indels: DNA sequence SeqI	Conservative: Mismatches: Indels:	ative: hes: cDNA
W09914241-A2. 25-MAR-1999. (GETH ) GENENTECH INC. recent Similarity: 80.17\$ ery Match: 25.45\$ SULT 1157 MAA95305 standard; CDNA; 1626 Murine CRAM-2 coding sequence.	rce at sur sur	PD 25-MAR-1999.  PA (GETH ) GENENTECH INC.  Best Local Similarity: 100.00\$  Query Match: 25.06\$  RESULT 1159  ID AAX56526 standard; DNA; 220 BP  DE Human 1508565 DNA Fragment.  PN W09914241-A2.	PD 25-MAR-1999.  Percent Similarity: 100.00\$  Best Local Similarity: 100.00\$  Query Match: 25.06\$  RESULT 1160  ID ABL39691 standard; CDNA; 980 BP.  DE Human NS CDNA sequence SEQ ID NO:10  PN WC20026315-A2.  PD 24-JAN-2002.	(COMP-) COMPUGEN LTD. rcent Similarity: 49.02% rcent Similarity: 33.33% rry Match: 24.94% rur 1161 AAL51600 standard; DNA; 93 Human junctional adhesion WG200300851-A2.	rce at ery sur	(GENE-) GENE LOGIC INC. (FPIZ ) PFIZER PROD INC. (FPIZ ) SA 198\$  The Local Similarity: 37.91\$  STY Match: 23.67\$  AAS28795 standard; CDNA; 367 E  Human immunoglobulin encoding	Proceed Similarity: 79.65% Conserving Match: 23.61% Indels: RESULT 1164 Indels: CDNA, 367 BP. CONSERVING Best Local Similarity: 67.26% Mismatci Query Match: 23.61% Indels: Indels: Indels: DE Human reproductive system related antigen

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25-MAR-1999
                                                                                                                                                                                                                                                                    Query Match:
RESULT 1182
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RESULT 1181
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RESULT 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human junction adhesion molecule 3 splice variant 2 (huJAM3sv2) cDNA.
WO2004053058-A2.
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Mismatches:
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAK92353 standard; cDNA; 824 BP.
Human cDNA 5'-end sequence, SEQ ID NO: 813.
EP1130094-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match: 21.05% Indel RESULT 1178

ID ADG3948 standard; cDNA; 714 BP.
DE Human JAM-2 encoding cDNA SEQ ID NO:17.
PN WO2003104400-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
RESULT 1176
ID ADP56688 standard; CDNA; 798 BP.
DE Human junction adhesion molecule 3
PN WO2004653058-A2.
PD 24-JUN-2004.
PA (FLIL ) LILLY & CO ELI.
Percent Similarity: 32.91%
Best Local Similarity: 32.91%
DE ..
PN EP14*.
PN ERST. RES. AS..
PD 28-JUL-20..
PA (REAS-) RES AS..
Percent Similarity:
Best Local Similarity: 28...
Query Match: 22.77$
RESULT 1173
ID AAX56507 standard; DNA; 257 BP..
Human 1299110 DNA fragment.
"19914241-A2."
"R-1999."
"R-1999."
"R-1999."
"R-1999."
"R-1999."
"R-1999."
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RESULT 1175
ID AAXS6513 standard; DNA; 257 BP.
DE Human 492141 DNA fragment.
PN W09914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADF12430 standard; cDNA; 714 BP
                                                                                                                                                                                                                                                                               AAX56527 standard; DNA; 191 BP.
Human 1508552 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PN WO2003087128-A2.
PD 23-OCT-2003.
PA (RMFD-) RMF DICTAGENE SA.
Percent Similarity: 48.318
Best Local Similarity: 33.058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PN WO2003104400-A2.
PD 18-DEC-2003.
PA (RMFD-) RMF DICTAGENE SA.
PA (UYPE-) UNIV PENNSYLVANIA.
Percent Similarity: 33.05%
Best Local Similarity: 33.05%
                                                                                                                                                                                                                                                                                                                     PN NO.25-MAR.1999.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
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90.14%
21.63%
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31.27%
21.05%
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PA (HELL-) HELIX RES INST.
Percent Similarity: 45.4
Best Local Similarity: 31.2
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PA (GETH ) GENENTECH INC.

Percent Similarity: 90.

Best Local Similarity: 90.
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RESULT 1177
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RESULT 1179
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RESULT 1180
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ADP69097 standard; cDNA; 618 BP.
Human NOV2a mature extracellular domain encoding cDNA SEQ ID NO:67.
WO2004055158-A2.
Human cDNA clone representative sequence, SEQ ID NO: 1707. EP1130094-A2.
                                                                                                                                                                                                                                                                                                   5' end of a representative human cDNA cluster SeqID 1707.
EP1396543-A2.
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119
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119
31
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92
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92
4
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92
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Mismatches:
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Mismatches:
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Mismatches:
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Mismatches:
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Mismatches:
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PN WO2D04055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 51.27% Conservat Best Local Similarity: 34.01% Mismatche Query Match: 19.75% Indela-
                                                                                                                                      ADL20780 standard; cDNA; 824 BP.
5' end of a human cDNA molecule SegID 813
EP1396543-A2.
                                                                                                           Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAIS9317 standard; cDNA; 561 BP.
Human polynucleotide SEQ ID NO 1520.
WO200153312-A1.
                                                                                                                                                                             PN BELLOMAR-2004.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 45.45%
Best Local Similarity: 31.27%
                                                                                                                                                                                                                                                                                                                        PN BELLOUAR-2004.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 45.45%
Best Local Similarity: 31.27%
                                                                                                                                                                                                                                                                                      ADL29674 standard; cDNA; 824 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADP69028 standard; cDNA; 637 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match: 19.75*
RESULT 1188
ID AAX56501 standard; DNA; 303 BP.
                                                                                                                                                                                                                                                                                                                                                                                               Query Match: 21.05%
RESULT 1183
ID AAX56506 standard; DNA; 259 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N mczcz---
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 51.27%
Best Local Similarity: 34.01%
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human 3234064 DNA fragment WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 51.27%
Best Local Similarity: 34.01%
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98.51%
20.66%
                                                                        Percent Similarity: 45.45%
Best Local Similarity: 31.27%
Query Match: 21.05%
                                                           (HELI-) HELIX RES INST.
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Percent Similarity: 98.
Best Local Similarity: 98.
Query Match: 20.
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AAX37665 standard; cDNA; 413 BP.
Human PRO protein derived EST consensus sequence DNA30954.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                            ABX93489 standard; cDNA; 413 BP.
Consensus sequence expressed sequence tag, EST, DNA30954.
US2002182206-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cDNA differentially expressed in colon cancer #43 US2002160382-A1.
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Mismatches:
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Mismatches:
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Mismatches:
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Indels:
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RESULT 1200
ID ADN31306 standard; DNA; 413 BP.
DD Human PRO245 consensus DNA fragment DNA30954.
PN WO2004031105-A2.
                                                                                                                                  Indels:
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Human A33 antigen (from clone 18)
WO9708189-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 1203
ADA10946 standard; cDNA; 1556 BP
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PD 60-MAR-1997.

PA (LUDM-) LUDWIG INST CANCER RES.

Percent Similarity: 42.58%

Best Local Similarity: 26.13%
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Human 777818 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADH62554 standard; DNA; 413 BP.
Human DNA30954 consensus DNA.
                                                                                                                                                                                                                          PD 25-MAR-1999.

PD 25-MAR-1999.

PAC (GETH ) GENENTECH INC.

Percent Similarity: 58.91%

Best Local Similarity: 47.29%

17.91%
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PD 25-MAR-1999.

Percent Similarity: 83.82%

Best Local Similarity: 82.35%
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47.29%
17.91%
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PARCENT SIMILARITY: 58.91%
Best Local Similarity: 47.29%
Anarw Match: 17.91%
                                                                                   58.91%
47.29%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity: 58 91%
Best Local Similarity: 47.29%
Query Match: 17.91%
                                            03-JUN-1999.
(GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                             05-DEC-2002.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ASHK) ASHKENAZI A.
(FONG) FONG S.
(GODD), GODDERD A.
(GURN) GURNEY A L.
(NAPI) NAPIER M A.
                                                                                                             Local Similarity:
                                                                                                                                                                                                                                                                                                                                                       RESULT 1198
ID ABX93489 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-OCT-2002.
(LASE/) LASEK A W.
(JONE/) JONES D A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TUMA/) TUMAS D. (WOOD/) WOOD W I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS2003171568-A1.
                  PN W09927098-A2.
PD 03-JUN-1999.
PA (GETH ) GENENTE Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
RESULT 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (huJAM3sv1) cDNA.
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RESULT 1196
ID AAX81783 standard; DNA; 413 BP.
DE Consensus sequence DNA30954 encoding an A33 related antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35
100
15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1191
ID ADP56687 standard; cDNA; 690 BP.
DE Human junction adhesion molecule 3 splice variant 1
PN WO2004053058-A2.
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12
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DNA encoding novel human diagnostic protein #22392.
                                                                                                             m 01 01
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Mismatches:
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Mismatches:
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Mismatches:
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DE WO95.
PN WO95.
PN ARR.15.
PA (GETH ) GENEN..
Percent Similarity.
Best Local Similarity: 90.1.
Query Match: 19.43*
RESULT 1189
ID AAX56511 standard; DNA, 227 BP.
Human AA227408 DNA fragment.
"O9914241-A2.
"R-1999.
"R-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT62383 standard; DNA; 2202 BP.
Mouse A33 antigen.
WO9708189-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD 06-MAR-1997.

PA (LUDW-) LUDWIG INST CANCER RES.

Percent Similarity: 47.35%

Best Local Similarity: 29.55%
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Human AA101519 DNA fragment.
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                 AAX56536 standard; DNA; 198 BP.
Human 1610836 DNA fragment.
WO9914241-A2.
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29.55%
18.43%
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94.12%
18.33%
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93.94%
18.01%
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Percent Similarity: 48.43%
Best Local Similarity: 32.74%
Query Match: 18.91%
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(GETH ) GENENTECH INC.
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PD 25-MAR.1999.
PA (GETH ) GENENTECH INC.
Percent Similarity: 93.8
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Percent Similarity: 94.
Best Local Similarity: 94.
Query Match: 18.
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PD 11-OCT-2001.
PA (HYSE.) HYSEQ INC.
Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                     Query Match:
RESULT 1190
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Best Local Similarity: 25.81% Mismatches: 123 Query Match: 17.65% Indels: 55	Human PRO cDNA sequence SEQ I WOZDO4039956-A2. 13-MAY-2004. (GETH ) GENENTECH INC. (GETH ) GENENTECH INC. 25-81% 12 Local Similarity: 25.81% 17.65%	ID ADK52877 standard; DNA; 2793 BP.	0 standard; DNA; 167 A404390 DNA fragment. 41-A2. GENENTECH INC. Larity: 100.00\$ imilarity: 17.62\$ 6 standard: CDNA: 748	DE Human CDNA 5'-end sequence, SEQ ID NO: 286.  PN EP1130094-A2.  PD 05-SEP-2001.  PA (HELI-) HELIX RES INST.  Percent Similarity: 32.74* Mismatches: 105  Query Match: 17.55* Indels: 11	RESULT 1216  ID AAK9326 standard; CDNA; 748 BP.  DE Human CDNA clone representative sequence, SEQ ID NO: 1686.  PN EF1310094-A2.  PD 65-SEP-2001.  PA (HELI-) HELIX RES INST.  Percent Similarity: 48.43*  Mismatches: 105	17.55% Indels: 17.55% Indels: 1 cDNA molecule SeqID 286. 2 BIOTECHNOLOGY. Conservative.	Dest Local Similarity: 32.74% Mismatches: 105 Ouery Match: 17.55% Indels: 11 RESULT 1218 ID ADL29635 standard; CDNA, 748 BP. DE 5' end of a representative human CDNA cluster SeqID 1686. PD 10-MAR-2004.	PA (REAS.) RES ASSOC BIOTECHNOLOGY. PA (REAS.) RES ASSOC BIOTECHNOLOGY. Percent Similarity: 48.43* Conservative: 35 Percent Similarity: 32.74* Mismatches: 105 Query Match: 17.55* Indels: 11 RESULT 1219 ID ADEE28280 standard; DNA; 1625 BP. DE Human MDDT DNA - SEQ ID 130. PN WO2003046152-A2.
Conservative: 52 Mismatches: 123 Tradi	ative: hes:	DP.  Conservative: 52  Mismatches: 123 Indels: 55  BP. ID NO: 68.	Conservative: 52 Mismatches: 123 Indels: 55 BP. CDNA sequence SEQ ID NO:276.	Conservative: 52 Mismatches: 123 Indels: 55 sequence SEQ ID NO:791.	Conservative: 52 Mismatches: 123 Indels: 55	expressed in granulocytic cells #1016.  Conservative: 52 Mismatches: 123 Indels: 55	cancer. Conservative: 52 Mismatches: 123	acid
Percent Similarity: 42.58% Best Local Similarity: 25.81%	9 standard; 33 antigen. 89-Al. 1997. LUDWIG INS; imilarity:	0 standard; cDNA; 2760 8424-A2. 2002. HYSEQ INC. HYSEQ INC. 10 12 12 17 17 17 17 17 17 17 17 17 17 17 17 17	28-DEC-2000.  (MILL-) MILLENNIUM PHARM INC.  (COLT Similarity: 42.58 tt Local Similarity: 25.81 tr.  PLY Match: 17.65 tr.  SLAH57436 standard; CDNA; 2793 Human intestine cell specific NORANA 2011.	Siry at	graft High	A differentially (A differentially 999-A2.) 002. 102. 103. 104. 105. 105. 105. 105.	ID ABN96940 standard; DNA; 2793 BP. DE Gene #3438 used to diagnose liver PN WO200229103-A2. PD 11-APR-2002. PA (GENE-) GENE LOGIC INC. PA (GENE-) GENE LOGIC SMR 42.58 Best Local Similarity: 25.81%	Ä 🖰

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Human prostate tumour protein partial DNA sequence #131.
US2002090372-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH02556 standard; cDNA; 382 BP.
Prostate tumour antigen determined cDNA sequence for
WO200125272-A2.
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US2002192763-A1.
                                                                                                                                                                                                                                           AAH93491 standard; cDNA; 382 BP.
Human prostate-specific cDNA sequence P185.
WO200151633-A2.
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Human prostate-specific cDNA sequence P185.
WO200134802-A2.
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Human prostate cDNA sequence #135.
WO200173032-A2.
         ABS71280 standard; cDNA; 382 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACA59392 standard; cDNA; 382 BP
ID ABS71280 standaru; c....,
DE Human prostate tumour protein
PN US2002090372-A1.
PD 11-UUL-2002.
PA (XUJJ/) XU J.
PA (DILL/) DILLON C.
Percent Similarity: 100.00%
Best Local Similarity: 16.39%
                                                                                                                                                                                                                                                                                          PN WO200151633-A2.
PD 19-UTL-2001.
PA (CORI-) CORIXA CORP.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 116.39%
RESULT 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAY-2001.
(CORI-) CORIXA CORP.
int Similarity: 100.00%
Local Similarity: 100.00%
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Best Local Similarity: 100.00%
Query Match: 16.39%
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Best Local Similarity: 100.00%
Query Match: 16.39%
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PA (FOYT/) FOY T M.
Percent Similarity: 100.00
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WANG A.
SKEIKY Y A.W.
HEPLER W T.
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KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
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DILLON D C.
MITCHAM J L.
HARLOCKER S 1
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HOUGHTON R L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARTER D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-OCT-2001
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RESULT 1332
DE ACC59392
DE PCOSTAGE
PN US200219;
PN US200219;
PN (19-DDC-20)
PA (MITC/) PA (MITC/
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RESULT 1228
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RESULT 1230
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WO200004149-A2.
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123
53
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18
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Mismatches:
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WO9837093-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV58612 standard; cDNA; 382 BP.
Prostate tumour specific gene clone.
WO9837418-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACH37074 standard; cDNA; 450 BP.
Human endothelial cell cDNA #5207.
US2003073623-Al.
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AAA06375 standard; cDNA; 382 BP.
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                                                                                          Query Match:
RESULT 1220
ID AAXS6537 standard; DNA; 237 BP.
DE Human 1274809 DNA fragment.
PN W09914241-A2.
                                                                                                                                                                                                                                                                                                                                                                    DNA; 198 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA; 204 BP.
  PD 05-JUN-2003.

PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 42.30%
Best Local Similarity: 25.57%
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PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
16.45$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PN WG927-AUG-1998.
PD 27-AUG-1998.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
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PD 27-AUG-1998.
PO CORI-) CORIXA CORP.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                      PD 25-MAR-1999.

PA (GETH ) GENENTECH INC.

Percent Similarity: 100.00$

Best Local Similarity: 17.10$
                                                                                                                                                                                                                   PD 25-MAR-1999.

PA (GETH ) GRNKBUTBCH INC.

100.00$

Best Local Similarity: 100.00$
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Best Local Similarity: 100.00%
Query Match: 17.10%
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Best Local Similarity: 100.00%
Query Match: 16.39%
                                                                                                                                                                                                                                                                                                                                                            AAX56533 standard; DNA; 190
Human 1519947 DNA fragment
WO9914241-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX56534 standard; DNA; 204
Human 1521745 DNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PD 27-JAN-2000.
PA (CORI-) CORIXA CORP.
Percent Similarity: 1
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                                                                                                                                                                                                                                                                                                                Query Match:
RESULT 1221
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RESULT 1227
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P185

Best Local Similarity: 1 Query Match: 1	100.00% 16.39%	Mismatches: Indels:	00
standard; ostate tum 5-Bl. 001. CORIXA COR arity: milarity:	CDNA, 382 BP.  OUT CDNA #25.  P.  100.00\$  100.39\$	Conservative: Mismatches: Indels:	000
standard; 85 cDNA se	DNA; 382 BP.	139.	
10.022248-A-10.0222602.  10.02	غ .		
CARTER D. LI S X. WANG A. WANG Y A HEPLER W T HENDERSON I arity: milarity:	W. ? A. 100.00% 16.39%	Conservative: Mismatches: Indels:	000
RESULI 1233  BE ABSS664 standard; cDNA; DE Prostate tumour cDNA #13 PN US2002081580-A1. PD 27-UN-2002. PA (XUJJ/) XU J. PA (DILL/) DILLON D C.	:DNA; 382 BP. 1 #135.		
arity: .milarity:	100.00% 100.00% 16.39%	Conservative: Mismatches: Indels:	
ID ACC95119 standard; cDNA; DE Prostate tumour specific PN W0200289747-A2.	:DNA; 382 BP. :ific cDNA sequence	SEQ ID 13	
002. CORIXA CORI arity: milarity:	p. 100.00% 100.00% 16.39%	Conservative: Mismatches: Indels:	
89 standard, prostate spec 185830-A1. -2003. ) CORIXA CORI ilarity: similarity:	cDNA; 382 BP. cific cDNA P185. p. 100.00% 100.00% 16.39%	Conservative: Mismatches: Indels:	000
RESULT 1238  ID ADG26005 standard; cDNA ADG26005 standard; cDNA DE Human prostate-specific PN US2003157089-A1.  PD 21-AUG-2003.  PA (CORI-) CORIXA CORP.  Percent Similarity: 100.0 elect Local Similarity: 100.0 elect Match:	; 382 BP. cDNA #135 00% 9%	Conservative: Mismatches: Indels:	000

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42
DE DNA encoding novel human diagnostic protein #22329.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Bercent Similarity: 55.92% Conservative: 25.92% Conservative: 25.92% Conservative: 25.92% Conservative: 25.92% Match:
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DB DNA encoding novel human diagnostic protein #12100.
DP N encoding novel human diagnostic protein #12100.
DP 11-0CT-2001.
PA (HYSE-) HYSEQ INC.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 50.68% Conservative: 26
Best Local Similarity: 15.88% Indels: 77
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Human PRO protein derived EST DNA sequence T89217.
WO9914241-A2.
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human diagnostic protein #4636.
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RESULT 1246

DE Human protein clone HP10568 full length coding in W020005357-A2.

PD 03-FEB-2000.

PA (SAGA) SAGAMI CHEM RES CENT.

PA (PROT-) PROFECENE INC.

PA (PROT-) PROFECENE INC.

PA (A3.73$ Mismatches: Best Local Similarity: 29.39$
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ID AAA15905 standard; CDNA; 981 BP.

DB Human protein clone HP10568 coding sequence. PN WO200005367-A2.

PD 03-FEB-2000.

PA (SAGA ) SAGAMI CHEM RES CENT.

PA (PROT-) PROTEGENE INC.

Percent Similarity: 43.73% Mismatches: Best Local Similarity: 29.39% Mismatches:
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ID AA191798 standard; CDNA; 403 BP. DE Human polynucleotide SEQ ID NO 11798. PN W0200164835-A2. DE Human polynucleotide SEQ ID NO 11798. PO 70-SEP-2001. PA (HYSE-) HYSEQ INC. B8.33% Conserved Similarity: 86.67% Mismatc Query Match: 15.58% Indels RESULT 1242

ID AASG8832 standard; CDNA; 15.39 BP. DE DNA encoding novel human diagnostic protop N W0200175067-A2. DE DNA (HYSE-) HYSEQ INC. Percent Similarity: 50.68% Mismatch Conserved Similarity: 32.88% Mismatch Conserved Conserved Similarity: 32.88% Mismatch Conserved Conserv
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DB Human 956595 DNA fragment.
DD MO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 15.74%
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DE Human PRO protein derived EST
D W09914241-A2.
PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Percent Similarity: 61.86*
Best Local Similarity: 15.06*
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ID AAS76296 standard;
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Query Match:
RESULT 1244
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RESULT 1240
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RESULT 1255	ADSOUST SCALLAGE, COMP. 1101 NOVEL human secreted and trans US2003088068-A1.	PA (GETH) GENENTECH INC. Percent Similarity: 43.73\$ Best Local Similarity: 29.39\$ Query Match: 15.03\$	ID ADB73372 standard; CDNA; 1161 BP. DE Novel human secreted and transmemb by reconstructions.	H INC	st Local Similarity: 29.39% ery Match: 15.03% SULT 1257	ID ADB78454 standard; cDNA; 1161 BP. DE Novel human secreted and transmemb PN US2003092889-Al. DD 15-MAV-2003	ž č	15.038	polynucleotide #118. 817-A1.	9 7 Y	ID AD978208 standard; cDNA; 1161 BP. DE Novel human secreted and transmemb by reconcions.	15-MAY-2003. (GETH ) GENENTECH	Percent Similarity: 43.73% Best Local Similarity: 29.39% Query Match: 15.03%	KESULI 1260 ID ADB87274 standard; cDNA; 1161 BP. DE Human PRO polynucleotide #118. DN 11620020602.31	08-MAY-2003. (GETH ) GENENTECH I	Percent Similarity: 43.73\$ Best Local Similarity: 29.39\$ Query Match: 15.03\$	RESULT 1261 ID ADB84856 standard, CDNA, 1161 BP. DE Human PRO polymucleotide #118.	US2003092890-A1. 15-MAY-2003. (GETH ) GENENTECH INC.	rcent Similarity: 43.73% Bt Local Similarity: 29.39% ery Match: 15.03% SULT 1262	ID ADB83971 standard; cDNA; 1161 BP. DE Novel human secreted and transmemb VN US20030683397-A1.	st st sury
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42		40 115	. 7		40 115 42	PRO7154 cDNA.	. 40	115 42		40 115	7		40 115	4.2 CDMR		40 115	42	A sequence.	40 115 42	PRO7154 cDNA.	40 115 42
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15.03%	DNA; 1161 BP. cein PRO7154 coding	NC. 43.73% 29.39%	CDNA, 1161 BP.	processis,	43.73% 29.39% 15.03%	cDNA; 1161 BP. d and transmembrane	<b>₩</b>	398 038	CDNA, 1161 BP.	7.3.9.4 3.9.4 4.0.4 4.0.4	os. A; 1161 BP.	!	* * *	1 BP.		.73 <b>%</b> 39 <b>%</b>	5.03 <b>%</b> DNA; 1161 BP.	receptor/prot	INC. 43.73% 29.39% 15.03%	AA; 1161 BP. and transmem	INC. 43.73% 29.39% 15.03%
Query Match: prent 1247	AAA91019 standard; Human secreted prot WO200075317-A2.	PD 14-DEC-2000. PA (GETH ) GENENTECH INC. Percent Similarity: 43.7 Best Local Similarity: 29.2	HELY MALCH: ESULT 1248 D ABK33653 standard; E CDNA encoding human	Ξ Ξ	rcent Similarity: st Local Similarity: sry Match:	RESULT 1249 ID ACA68614 standard; cDNA, DE Novel human secreted and PN HSOA1088061-A1	PD 08-MAY-2003. PA (GETH ) GENENTECH I Percent Similarity:	Best Local Similarity: 29. Query Match: 15.	ABT44343 standard; Human PRO7154 cDNA. US2003050448-A1.	PD 13-MAR-2003.  PA (GETH ) GENENTECH INC.  Percent Similarity: 43.  Best Local Similarity: 29.	6 standard;	PN US2003027988-A1. PD 06-FEB-2003.	PA (GETH ) GENENTECH INC. Percent Similarity: 43.7 Best Local Similarity: 29.3	Query Match: RESULT 1252 ID ACD82293 standard; DE Human secreted/tran	US200304	GENENTECH I larity: imilarity:	ery Match: SULT 1253 ABT43999 standard;	Human membrane bour US2003065147-A1.	(GETH ) GENENTECH ccent Similarity: st Local Similarity: erv Match:	5 standard; uman secret	PN 022020/301-AL. PD 17-APR-2003. PA (GETH ) GENENTECH I Percent Similarity: Best Local Similarity: Query Match:

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ane protein PRO7154 cDNA.

DE Novel human secreted and transmembra: PN US2003056972-A1. PD 22-MAY-2003. PA (GETH) GENERITECH INC. Percent Similarity: 43.73% Mi. Query Match: 1272 ID ADD06417 standard; cDNA; 1161 BP. DE Novel human secreted and transmembra: PD US2003073916-A1. PD T-APR-2003.	PA (GETH ) GENENTECH INC. Percent Similarity: 43.73% Coy Best Local Similarity: 29.39% Mis Query Match: 15.03% In. REGULT 1273 ID ADC77936 standard; CDNA; 1161 BP. DE Novel human secreted and transmembran PN US2003088066-Al. PD 08-MAY-2003. PA (GETH ) GENENTECH INC.	rcent Simil st Local Si ery Match: SULT 1274 ADD50895 Novel hu	PA (GETH) GENENTECH INC. Percent Similarity: 43.73% Co. Best Local Similarity: 29.39% Mis Query Match: 15.03% In RESULT 1275 ID ADD51145 standard; CDNA; 1161 BP. DE Novel human secreted and transmembran PN IG2003105290.A1.	PD 05-JUN-2003.  PA (GETH) GENENTECH INC. Percent Similarity: 43.73\$ Coy Best Local Similarity: 29.39\$ Mii Query Match: 15.03\$ In RESULT 1276 ID ADD50626 standard; CDNA; 1161 BP. DE Human PRO polymucleotide #118. PN US2003096971-A1.	£ 7 4 6	H INC. 43.73\$ 1.29.39\$ 15.03\$ 2; CDNA; 1161 BP. eted and transmemb H INC. 43.73\$	Best Local Similarity: 29.39% Mills Query Match: 15.03% In. RESULT 1279 ID ACA66958 standard; CDNA; 1161 BP. DE CDNA encoding human PRO polypeptide:
54 CDNA.		54 cDNA.	54 CDNA.	54 cDNA.	54 cDNA.	54 CDNA.	
transmembrane protein PRO7154 transmembrane protein PRO7154 Conservative: 40 Mismatches: 115 Indels: 42 1161 BP.	Conservative: 40 Mismatches: 115 Indels: 42 BP.	Conservative: 40 Mismarches: 115 Indels: 42 1161 BP. transmembrane protein PRO71	Conservative: 40 Mismatches: 115 Indels: 42 1161 BP.	Conservative: 40 Mismatches: 115 Indels: 42 1161 BP. transmembrane protein PRO71	Conservative: 40 Mismacches: 115 Indels: 42 1161 BP. transmembrane protein PRO7154	Conservative: 40 Mismatches: 115 Indels: 42 1161 BP.	Conservative: 40 Mismatches: 115 Indels: 42 BP.
cDNA; d and nC. 13, 13, 29.39, 15.03, cDNA; otide	3% 9% 3% 1161 = #118.	NC. 43.73\$ 29.39\$ 15.03\$ cDNA;	VC. 13.73% 29.39% LS.03% CDNA;	C. 33, 73, 99, 39, 39, 39, 39, 39, 39, 39, 39, 3	PN US2003088011-A1. PN US203088011-A1. PA 08-MAY-2003. PA (GETH) GENENTECH INC. Percent Similarity: 43.73\$ Best Local Similarity: 29.39\$ Query Match: 15.03\$ RESULT 1269 ID ADC47562 standard; CDNA; 1161 DE Novel human secreted and trans PN US2003088072-A1.	NC. 43.73% 29.39% 15.03% CDNA; cDNA;	73.73% 29.39% 15.03% cDNA; 1161

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PD 29-MAY-2003. PA (GETH) GENENTE Percent Similarity: Best Local Similarity Query Match: RESULT 1288	1D ADEZUB63 STANDAR NOVEL human Sec. PW US2003100734-A1 PD 29-MAY-2003 PA (GETH ) GENENTER	Percent Similarity: Best Local Similarity Query Match: RESULT 1289	1D ADESTED STANDADED DE NOVEL human sec: PN US200309642-A1 PD 22-MAY-2003.	it ce		rce sty	1D ADD/3592 SCANDARD DE Human PRO polynu PN US2003100711-A1 PD 29-MAY-2003	rcent Simil st Local Si ery Match: SULT 1292		rcent Simil st Local Si ery Match: SULT 1293		PA (GETH) GENERITE Percent Similarity: Best Local Similarity: Query Match: RESULT 129 ID ADD74470 standan		rcent Simi) st Local Si sry Match: SULT 1295	DE Novel human sections of the Novel human sections Novel human sections Novel human sections OF 29-MAY-2003.
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Conservative: Mismatches: Indels:	1161 BP. transmembrane protein	Conservative Mismatches: Indels:	1161 BP. transmembrane protein PRO7154	Conservative Mismatches: Indels:	1161 BP. transmembrane protein PRO7154	Conservative Mismatches: Indels:	1161 BP. #118.	Conservative: Mismatches: Indels:	1161 BP. #118.	Conservative: Mismatches: Indels:	1161 BP. transmembrane pı	Conservative: Mismatches: Indels:	1161 BP. transmembrane protein PRO7154	Conservative: Mismatches: Indels:	1161 BP. transmembrane pr
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PN US2003036635-A1. PD 20-FEB-2003. PA (GETH) GENENTECH PETCENT Similarity: Best Local Similarity: Query Match.	ACD68710 standard NOVel human secret US2003045687-A1.	PA (GETH ) GENENTECH Percent Similarity: Best Local Similarity: Query Match: RESHLT 1281	ID ADC48938 standard, CDNA, DE Novel human secreted and PN US2003092888-A1.	15-MAY-2003. (GETH ) GENENTECH ccent Similarity: st Local Similarity: sry Match:	ID ADE21109 standard; cDNA; DE Novel human secreted and PN US2003100735-A1.	29-MAY-2003. (GETH ) GENENTECH (Cent Similarity: st Local Similarity: rry Match:	ID ADE05953 standard, cDNA, DE Human PRO polynucleotide PN US2003100728-A1. PD 24-MAY-2003	(GETH ) GENENTECH cent Similarity: st Local Similarity: sry Match:	ID ADD75182 standard; cDNA; DE Human PRO polynucleotide PN US2003100712-A1. PD 29-MAY-2003.	# # K	ID ADD75928 standard; cDNA; 1161 BP. DE Novel human secreted and transmembrane protein PRO7154 PN US200100717-A1.	PA (GETH ) GENENTECH INC. Percent Similarity: 43.73* Best Local Similarity: 29.39* Query Match: 15.03* RESULT 1286	ID ADD85160 standard; cDNA; DE Novel human secreted and PN US2003100722-A1. PD 29-MAY-2003	1 t G	ID ADD86986 standard; DE Novel human secret: PN US2003100738-A1.

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	conna, 1161 BP. lectide #118. INC. 43.73* 29.39* 15.03*	cobide #118. lectide #118. INC. 29.39* 15.03*	; cDNA; 1161 BP. leotide #118. INC. 29.39 15.03\$	cDNA;	INC. 43.73% 29.39% 15.03%		INC. 43.73% 29.39% 15.03%	cotide #118. cotide #118. INC. 43.73% 29.39% 15.03%	; cDNA; 1161 BP. lectide #118. INC. 43.73%	
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ADD77962 standard; cDNA; 1161 BP.
Novel human secreted and transmembrane protein PRO7154 cDNA.
US2003100730-A1.
                           iry March:

15.03* Indels: 42

SULT 1304

ADD86740 standard; cDNA; 1161 BP.

Novel human secreted and transmembrane protein PRO7154 cDNA.

US2003100719-A1.
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SULT 1306
ADD77716 standard; cDNA; 1161 BP.
Novel human secreted and transmembrane protein PRO7154 cDNA.
US2003100729-A1.
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ADD85420 standard; cDNA; 1161 BP.
NOVEL human secreted and transmembrane protein PRO7154 cDNA.
US2003100725-A1.
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Novel human secreted and transmembrane protein PRO7154 cDNA.
US2003100731-A1.
29-MAY-2003.
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Human PRO polynucleotide #118.
US2003100710-A1.
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Query Match:	1D ADG06/97 DB Human PRC PN US2003096 PD 22-MAY-20	g # g P	1D ADM35141 DE Novel hun PN US2003096 PD 22-MAY-20	art e	1D ADG34231 DE Novel hun PN US2004006 PD 08-JAN-20 PA (GETH )	Percent Simil Best Local Sin Query Match: RESULT 1323	DE Human PRC PN US2003096 PD 22-MAY-20	PA (GETH ) GERH ) G Percent Simila Best Local Sim Query Match: RESULT 1324	1D ADH69/95 DE Human PRC PN US2004019 PD 29-DAN-20 PA (GETH )	g 7 7 g	1D AD12998 DE Novel hum PN US2003096 PD 22-MAY-20	g 7, 7, 2		PA (GETH ) G Percent Simila Best Local Sim Query Match: RESULT 1327	Human PF US200404 04-MAR-2	PA (GETH ) G Percent Simila Best Local Sim Query Match:
S	154 cDNA.	10					154 cDNA.				154 CDNA.	10	.54 cDNA.		.54 cDNA.	
Mismatches: 119 Indels: 42	rane protein PRO7154	Conservative: 40 Mismatches: 115 Indels: 42		Conservative: 40 Mismatches: 115 Indels: 42		Conservative: 40 Mismatches: 115 Indels: 42	1161 BP. transmembrane protein PRO7154	Conservative: 40 Mismatches: 115 Indels: 42		Conservative: 40 Mismatches: 115 Indels: 42	rane protein PRO71	Conservative: 40 Mismatches: 115 Indels: 42	1161 BP. transmembrane protein PRO7154	Conservative: 40 Mismatches: 115 Indels: 42	1161 BP. transmembrane protein PRO7154	Conservative: 40 Mismatches: 115
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Best Local Similarity: Query Match:	RESULT 1312 ID ADD85912 standard; CDN DE Novel human secreted PN US2003100720-A1.	PD 25-MAY-2003. PA (GETH) CENENTECH PErcent Similarity; Best Local Similarity; Query Match:	TESOLI 1913 1D ADBOS461 standard; CDNA; 1161 BP DE Human PRO polynucleotide #118. PN US2003100723-A1. PN 92-MAY-2003	(GETH) GENENTECH coent Similarity: st Local Similarity:	6 standard; RO polynucl 00724-Al. 2003.	(GETH ) GENENTECH cent Similarity: it Local Similarity: sry Match:	ID ADG05748 standard; cDNA; DE Novel human secreted and PN US2003096959-A1.	-2003. GENENTECH ilarity: Similarity:	RESULI 1316 ID ADG27302 standard; DE Human PRO polynucl PN US2003096962-A1. PD 22-MAY-2003.	円に	RESOLD 13.1 DE MOOS1365 standard; CDNA; 1161 BP. DE Novel human secreted and transmembrane protein PRO7154 PN US203095667-A1. PD 22-MAV-2003	(GETH ) GENENTECH coent Similarity: st Local Similarity: rry Match:	KESULI 1318 ID ADG12144 standard; CDNA; DE Novel human secreted and PN US2003096963-A1.	<pre>22-mAT-2003. (GETH ) GENENTECH ccent Similarity: st Local Similarity: sty Match: n 1210.</pre>	1D ADP94701 standard; cDNA; DE Novel human secreted and PN US2003096964-Al.	PD 22-MAY-2003. PA (GETH ) GENENTECH INC. Percent Similarity: 43. Best Local Similarity: 29.

	Query Match:	15.03%	Indels: .	42
	7 standard; RO polynucl	cDNA; 1161 BP. eotide #118.		
	022003036966-A1. 22-MAY-2003. (GETH ) GENENTECH	NC.		
	Percent Similarity: Best Local Similarity: Query Match:	43.73% 29.39% 15.03%	Conservative: Mismatches: Indels:	40 115 42
	RESULT 1321 ID ADH39141 standard; cDNA, DE Novel himan secreted and	CDNA; 1161 BP.	r.	PP.07154
	US2003096965-A1. 22-MAY-2003.	4		•
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	1 standard;	CDNA; 1161 BP.		
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•	Human PRO polynucle	ide #118.		
	29-JAN-2004.	ţ		
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	Query Match: RESULT 1325	.5.03%	Indels:	42
	ID ADI29956 standard; c	cDNA; 1161 BP.	nrotein	DRO7154 CDNA
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		3.73%	Conservative:	40
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	RESULT 1326 ID ADM27353 standard.			
	DE Novel human secrete	d and transmembrane	protein	PRO7154 cDNA.
	PN US2004044179-A1. PD 04-MAR-2004.			
	(GETH ) GENENTECH	-		;
	larity: imilarity:	43.73%	Conservative: Mismatches:	40 115
			Indels:	42
	DE Human DRO nolvanicleoride	CDNA; 1161 BP.		
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DE Human signal peptide containing protein HSPP-28 cDNA SEQ ID NO:162.

PN WCOCONO610-A2.

PD 06-JAN-2000.

PA (INCY-) INCYTE PHARM INC.

Percent Similarity: 43.73% Conservative: 40

Best Local Similarity: 29.33% Mismatches: 115

Query Match: 15.03% Indels:
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Human corticol thymocyte receptor CTXL, overexpressed in cancer.
WO2003100000-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human diagnostic and therapeutic polynucleotide SEQ ID NO:2386 WO2004023973-A2.
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DE Human COLO...
PN WOZDO055351-A1.
PN WOZDO055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43-73% Mismatches: 115
Query Match: 15.03% Indels: 42
RESULT 1330
ID AAH35018 standard; CDNA; 1186 BP.
DE Human Colon cancer antigen encoding cDNA SEQ ID NO:2100.
PN WOZO0122920-A2.
PN 
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AAC98064 standard; cDNA; 1186 BP.
Human colon cancer antigen nucleotide sequence SEQ ID NO:74.
WO200055351-A1.
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Human polynucleotide SEQ ID NO 1325.
WO200190304-A2.
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DE Human polynucleotide SEQ ID NO 1
PN W0200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.73*
Best Local Similarity: 29.39*
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DE Human secreted protein gene 13
PN W020001722-A1.
PD 30-MAR-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.37%
Rest Local Similarity: 29.39%
Query Match:
RESULT 1335
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PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Query Match: 1336
RESULT 1336
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DE Human diagnostic and therape
PN WO200402373-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Percent Similarity: 43.94%
Query Match: 1333
RESULT 1333
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DE Human corticol thymocyte ree
PN WO2003100000-A2.
PD 04-DEC-2003.
PA (TULA-) TULARIK INC.
Percent Similarity: 28.81%
Best Local Similarity: 28.81%
Query Match: 14.83%
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Human 2861301 DNA fragment.
WO9914241-A2.
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RESULT 1332
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RESULT 1329
RESULT 1328
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Angiogenesis inhibitor human DNA sequence, GS-N52.
FR2843753-A1.
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Mismatches:
AAA39087 standard; cDNA; 1135 BP.
Human secreted protein gene 13 SEQ ID NO:46.
WO200017222-A1.
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                                                                                                                                            ABXS6303 standard; DNA; 8243 BP.
Human NOV25b CG93858-02 DNA SEQ ID 85.
WO200281625-A2.
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RESULT 1342
ID AD008272 standard; cDNA; 15659 BP.
DE Human NOVX polynucleotide #10.
PN US2004018594-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADS09799 standard; DNA; 8546 BP.
Human therapeutic DNA - SEQ ID 36.
 ID AAA39087 standard; curr, class of Human secreted protein gene 13 S PN WC200017222-A1.
PD 30-MAR-2000.
PA (HUMA-) HUMAN GENOME SCI INC. Percent Similarity: 43.73% Best Local Similarity: 13.92%
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADK60778 standard; DNA; 8546 BP.
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PN FR2836666-A1.

PN GENE-) GENE SIGNAL.

PA (GENE-) GENE SIGNAL.

PA (ALMA/) AL MAHMOOD S.

Percent Similarity: 38.98$

"Agt Local Similarity: 29.24$

"Atch: "Aard; DNA; 8F
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PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Per cent Similarity: 38.98*
Best Local Similarity: 29.24*
Lich:
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29.24%
13.89%
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Best Local Similarity: 29.24%
Query Match: 13.89%
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Best Local Similarity: 29.24%
Omery Match: 13.89%
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ANDERSON D W.
BOLDOG F L.
BURGESS C E.
CASMAN S J.
CHAPOVAL A.
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                                                                                                                                                                                             17-OCT-2002.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                               (GENE-) GENE SIGNAL.
(ALMA/) AL MAHMOOD S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PN FRZ843753-A1.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Percent Similarity: 3
Best Local Similarity: 3
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GERLACH V.
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Human thrombospondin protein, BTL.012, coding sequence.
W0200174852-A2
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81
63
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81
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DNA encoding novel human diagnostic protein #3924.
WO200175067-A2.
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WO2003102155-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human G-coupled protein receptor-related gene #44. US2004006205-A1.
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Mismatches:
Indels:
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Human NOVX polynucleotide #10.
WO200290504-A2.
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ADL93996 standard; cDNA; 5877 BP.
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RESULT 1346
ID AAI72024 standard; CDNA; 4073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PN WO200174852-AZ.
PD 11-OCT-2001.
PA (FARB) BAYER CORP.
Percent Similarity: 38.98%
Best Local Similarity: 29.24%
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (LILL/) LI L.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PATT/) PATTURAJAN M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (TAUP/) TAUPIER R J.
PA (VOSS/) VOSS E Z.
PA (VOSS/) VOSS E Z.
PA (COSS/) VOSS E Z.
PA (CONS) MILLET SIMILATILY: 29.24%
QUELY MATCH: 13.89%
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PA (CURA-) CURAGEN CORP.

Percent Similarity: 38.98*

Best Local Similarity: 29.24*

Local Similarity: 13.89*
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PACTORNAL SIMILARITY: 38.98 Best Local Similarity: 29.24 Ouerv Match: 13.898
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29.24%
13.83%
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MILLER C E.
SPYTEK K A.
ZERHUSEN B D.
PENA C E A.
SHENOY S G.
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SMITHSON G.
CASMAN S J.
BOLDOG F L.
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PA (HYSE-) HYSEQ INC.

Percent Similarity:

Best Local Similarity:
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GERLACH V.
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(CASM/)
(BOLD/)
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(MILL/)
(SPYT/)
(ZERH/)
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(SHEN/)
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1D ADE16657 standard; DNA; 5935 BP.
DB G-coupled protein receptor related polypeptide DNA, SEQ ID NO 87.
PN WC200283841-A2.
PD 24-0CT-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 38.98* Conservative: 23
Percent Similarity: 29.24* Mismatches: 81
Ouery Match: 13.83* Indels: 63
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Human gene of the invention NOV43d SEQ ID NO:1003.
WO2003102155-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADK60455 standard; DNA; 18207 BP.
Angiogenesis differentially expressed gene GS-N29.
FR2836687-Al.
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Angiogenesis differentially expressed gene GS-N29.
FR2836686-A1.
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Human NOV25c CG56914-03 DNA SEQ ID 87.
WO200281625-A2.
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ID ABQ86156 standard, DNA; 16908 BP.
DE NOVEL human gene. SEQ ID 27.
PN WO200250105-A1.
PD 27-JUN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 38 98%
Best Local Similarity: 29.24%
Query Match:
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PD 05-SEP-2003.

PA (GENE-) GENE SIGNAL.

PA (ALMAK) AL MAHMOOD S.

Percent Similarity: 38.98%

Best Local Similarity: 29.24%
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D 17-OCT-2002.
Percent Similarity: 38.98%
Best Local Similarity: 29.24%
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PD 11-DC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 38.98%
Best Local Similarity: 29.24%
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29.24%
13.83%
VOSS E Z.
VERNET C A.
MACDOUGALL J R.
                                                                                                                               PATTURAJAN M.
BURGESS C E.
MALYANKAR U M.
SHIMKETS R A.
TAUPIER R J.
                                                                   ANDERSON D W.
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(GENE-) GENE SIGNAL.
(ALMA/) AL MAHMOOD S.
                                                                                  ZHONG M.
MEZES P S.
FURTAK K.
                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                  (MALY) (SHIM/) (TAUP/) (TAUP/) (EDIN/) (MAZU/)
                                  (MACD/)
(RAST/)
(ANDE/)
(ZHON/)
                                                                                                                                   (PATT/)
(BURG/)
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23 81 63		23 81 63		41 124 42		41 124 42		47 114 49	(HCAR) cDNA.	42 109 49		47 114 49	на сDNA.	47 114 49	
Conservative: Mismatches: Indels:	sequence, GS-N25	Conservative: Mismatches: Indels:	SEQ ID No 72.	Conservative: Mismatches: Indels:	SEQ ID NO 72.	Conservative: Mismatches: Indels:	11.	Conservative: Mismatches: Indels:	BP. and Ad5 receptor (HC	Conservative: Mismatches: Indels:		Conservative: Mismatches: Indels:	r (CAR) encoding	GES MBH. Conservative: Mismatches: Indels:	
.98% .24% .83%		.98 8.48 8.38 8.38	DNA; 1853 BP. encoding cDNA SEQ		cDNA; 1853 BP. ; a novel protein SEQ	INC.	36 BP. A SEQ ID	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4		cDNA; 2434 BP.	CORP.	ONA; 2434 BP. Ovirus receptor	SRW	
larity: 38 imilarity: 29.	8 standard; nesis inhibi 53-A1. 2004. GENE S.	AL M S. larity: 38 imilarity: 29	1 1535 MAS28826 standard; cDNA; 1853 Human immunoglobulin encoding WO200155315-A2.	2001. HUMAN GENOME .larity: 46 similarity: 26	1 standard; DNA encoding 77606-A1.	ğ	6 standard; OV4a CG5987 1625-A2.	Ö	9 standard; oxsackievir 19-Al	1998. UNIV NEW YORK larity: 42. Similarity: 26.		$\stackrel{\smile}{\sim}$	22 standard; cl coxsackie-adenc 9072-A2.	2002. NOVARTIS AC NOVARTIS-EI larity: imilarity:	T 1361
Percent Similarity: Best Local Similarity Query Match:	TESOLI 1354 ID ADP73078 DE Angiogen PN FR284375 PD 27-FEB-2	(ALMS/) rcent Simi st Local S ery Match:	ID AAS2882 DE Human i	PD 02-AUG-2001. PA (HUMA-) HUMAN GENON Percent Similarity: Best Local Similarity: Query Match:	RESULT 1356  ID ADB3155  DE Human c PN US20030	at.	RESULT 1357 ID ABX5626 DE Human N	3 2 2	RESULT 1358 ID AAV5042 DE Human c	iry Ty	RESULT 1359 ID AAC8581 DE Human C PN US62459	PD 12-UN-2001. PA (UYTE-) UNIV TECHN Percent Similarity: Best Local Similarity: Query Match:	RESULT 1360 ID ABL6062 DE Human c PN WO20022	PD 11-APR-2002 PA (NOVS ) NOVARTIS PA (NOVS ) NOVARTIS PERCENT SIMILARILY; Best Local Similarity Query Match:	RESULT 1361

WO2004065545-A2. 05-AUG-2004.

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Human breast cancer / ovarian cancer related coding sequence #39.
WO2003000012-A2.
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RESULT 1368
ED MILL 1368
DE Human angiogenesis related cDNA PRO5723 SEQ ID NO: 279.
PN W0200208284-A2.
PD 31-JAN-2002.
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114
49
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Percent Similarity: 42.40$ Mismatches: 114
Best Local Similarity: 42.40$ Mismatches: 116
Cuery Match: 13.44$ Indels: 49
RESULT 1362
ID ADRESSIS standard; DNA; 2434 BP.
DE Human prostatic carcinoma derived DNA SEQ ID 25 #3.
PA (HINZ) HINZMANN B.
PA (HIRZ) PILARSKY C.
PA (HIRZ) PILARSKY C.
PA (HIRZ) PILARSKY C.
PA (HIRZ) PILARSKY C.
PROSED Standard; DNA; 2434 BP.
DE Human prostatic carcinoma derived DNA SEQ ID 25 #1.
PA (PILA/) PILARSKY C.
PROSED Standard; DNA; 2434 BP.
DE Human prostatic carcinoma derived DNA SEQ ID 25 #1.
PA (HINZ) HINZMANN B.
PA (HINZ) HINZMANN B.
PA (HINZ) HINZMANN B.
PA (HIRZ) PILARSKY C.
PROSED STANDARSKY C.
PA (HIRZ) PILARSKY C.
PA (HIRZ) PILARS
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ID ADM95227 standard; DNA; 2537 BP.

DE Human BEC/LEC-related gene sequence SeqID149. PD 02-0CT-2003. PA (LUDW-) LUDWIG INST CANCER RES. PA (LUCW) LICENTIA LTD. PA (LICW) LICENTIA LTD. PERCENT Similarity: 25.80% Mismatches: Query Match: 13.44% Indels: Indels:
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WO200200690-A2.
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RESULT 1367
ID ABL88211 standard; cDNA; 2940
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07-NOV-2002.
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RESULT 1365
ID ABV76135
DE Coxsackie
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US2003017476-A1
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RESULT 1382
ID ABX17256
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RESULT 1377
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RESULT 1381
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       RESULT 1375
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Novel human secreted and transmembrane protein PRO5723 cDNA.
US2003003531-A1.
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Human PRO5723 nucleotide sequence SEQ ID NO:504
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cDNA encoding human PRO protein, Seq ID No 215.
WO200208288-A2.
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Human DNA82361 cDNA encoding PRO5723.
US2002192752-A1.
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ID AAD02924 standard; cDNA; 3060 BP.
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ID AAC91489 standard; cDNA; 3060 BP.
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WO200116319-A2.
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PD 19-DEC-2002.
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(GETH ) GENENTECH INC.
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PA (GETH ) GENENTECH INC.

Percent Similarity: 42.

Best Local Similarity: 25.
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MARSTERS S A.
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(WILL/) WILLIAMS P M.
(WOOD/) WOOD W I.
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STEPHAN J F.
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PD 02-JAN-2003.
PA (GETH) GENENTECH IN
Percent Similarity: 4
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WO200073452-A2.
                                                         FERRARA N.
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ACA68604 standard; cDNA; 3060 BP.
Novel human secreted and transmembrane protein PRO5723 cDNA.
US2003088063-A1.
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US2003022187-A1.
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Novel human secreted and transmembrane protein PRO5723 cDNA.
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Novel human secreted and transmembrane protein PRO5723 CDNA.
US200217714-A1.
28-NOV-2002.
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Novel human secreted or transmembrane protein PRO3301 DNA.
US2003027985-A1.
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ABX80973 standard; cDNA; 3060 BP.
Human secreted/transmembrane protein cDNA, #177.
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CODA encoding human PRO5723 polypeptide.
US2002127576-A1.
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Local Similarity: 25.80%

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PN US2003027162-A1.
PD 06-FEB-2003.
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	best Local Similarity: 25.80% Query Match: 13.44% RESULT 1419 1D ADC36944 standard; cDNA; DE Human PRO polynucleotide	PN 02204308805-A1. PD 08-MAY-2003. PA (GETH) GENENTECH : Percent Similarity: Guery Match: RESULT 1420	4 standard; RO polynucl 96969-A1. 2003. GENENTECH Iarity: imilarity:	5 standard uman secret 88064-Al. 2003.	(GENEAL CENERALECH COENT SIMILARITY: St Local Similarity: COENT MATCH:	ESOLIA TATE.  ID ADC49164 standard; CDNA;  DE Novel human secreted and PN US2003088070-A1.	GENENTECH ilarity: Similarity:	RESUL 1413 ID AD049681 standard, CDNA, DE Novel human secreted and PN US2003088071-A1.	(GETH ) GENENTECH cent Similarity: Bt Local Similarity: STY Match:	AESOLI 1427 DE ADC47542 standard; CDNA; DE Novel human secreted and PN US2003088072-A1. PD 08-MAY-2003.	PA (GETH) GENENTECH Percent Similarity: Best Local Similarity: Query Match: PESTITY 1435	1D ADC14804 standard, cDNA, DE Novel human secreted and PN US2000308246-A1.	ity it	ID ADC47287 standard; cDNA; DE Novel human secreted and

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DD51371 standard, cDNA, 3060 BP. fovel human secreted and transmembrane protein PRO5723 cDNA. IS2003105289-A1.
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Numan cDNA encoding secreted/transmembrane protein PRO5723.
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Human secreted/transmembrane PRO polypeptide cDNA #140.
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tuman PRO polynucleotide #108.
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Best Local Similarity: 25.80% Query Match: 13.44% RESULT 1452 ID PAP67431 standard; CDNA; 3 DE Human PRO5723 nucleotide BN 923002198148-A1.	PA (GETH) GENERICH DE GENERAL SIMILARITY: Best Local Similarity: Query Match: RESULT 1453	ID ADE94084 standard; cDNA; 3060 BP. DE Immune disease treatment/diagnosis related PN US2003082199-A1.	PA (GETH ) GENENTECH INC. Percent Similarity: 42.40% Best Local Similarity: 25.80% Query Match: 13.44% RESULT 1454 ID AD135685 standard; cDNA; DE Human PRO polynucleotide PN US2003050457-A1.	PD 13-MAR-2003. Percent Similarity: Best Local Similarity: Query Match:	ID ADIO178 standard; c DE NOVel human secreted PN US2003049682-A1.	PD 13-MAR-2003. Percent Similarity: Best Local Similarity: Query Match:	7 standard, RO polynuc] 27163-A1.	arity: nilarity:	RESULT 1457  ID ABX80469 standard; DNA; DE Novel human secreted or PN US200213252-A1.	SENENTECH arity: nilarity:	ACA69375 standard; cDNA; 3060 BP. Human cDNA encoding secreted/transmembrane protein PRO5723 US2003032023-A1.	PD 13-FEB-2003. Percent Similarity: Best Local Similarity: Query Match:	T 1459 ABX90446 standard; Human secreted/trar US2002160384-Al.	PA (GETH) GENENTECH INC. Percent Similarity: 42.40% Conserva' Best Local Similarity: 25.80% Mismatch Query Match: 13.44% Indels:	ACA66948 standard; cDNA; 3060 BP. CDNA encoding human PRO polypeptide #108
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1477

1077450 standard; CDNA; 3060 BP.

vol human secreted and transmembrane protein PRO5723 CDNA.
2003100732-A1.

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cal Similarity: 25.80% Mismatches: 114

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S9-MAY-2003.

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-Q=/cgn2_1/USPTO_epool/US1078520.rst -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bite -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500
-UNITS=bite -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500
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-USFR=US10785220 @CGN 1 1 3437 @runat_07092005_161055_17745 -NCPU=6 -ICPU=3
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-FGAPORT=120 -WARN TIMEOUT=30 -TRIREADS=1 -XGAPOP=10 -XGAPORT=0.5 -FGAPOP=6
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd

    nucleic search, using frame_plus_p2n model

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Genoscope.

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCWNSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
21-JUL-2004
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                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1594)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
Unpublished
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full-length cDNA clone CS0DI075YL24 of Placenta Cot 25-normalized
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                                                                                                                                                          Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Homo sapiens (human)
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/note="lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized.
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31271441
Contact: Genoscope
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Location/Qualifiers
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AL549523 Homo sapiens PLACENTA COT 25-NORMALIZED Holone CSODIO55YH06 5-PRIME, MRNA sequence.
AL549623.3 GI:45750009
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BM548873 1020 bp mRNA linear EST 20-FEB-2002 AGENCOURT 6543385 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5740989 5', mRNA Sequence.
BM548873.1 GI:18783816
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1. (bases 1 to 1020)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ArC

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12756 row: m column: 22
High quality sequence stop: 666.
Location/Qualifiers
                  201 ProLeuSerAlaSerAspThrGlyGluTyrSerCysGluAlaArgAsnGlyTyrGlyThr
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqretégenoscope.cns.fr, Web : www.genoscope.cns.fr, Web : www.genoscope.cns.fr, Web is trand cDNA was primed with a NotI-oligo dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster. For more information about this cluster, see http://www.genoscope.cns.fr/cdna?e=CSODL004CB02QP1&c=250.r.
Location/Qualifiers
                                                                                                AL560725
AL560725 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED Homo sapiens CDNA clone CSODL004YD03 5-PRIME, mRNA sequence.
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1 (Bases 1 to 993)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

On Peb 15, 2001)

On Peb 15, 2001 this sequence version replaced gi:31284854.

Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pcMVSPORT 6 vector. Library was normalized."
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25-NORMALIZED"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

12. (Mases 1 to 1034)

13. (Mases 1 to 1034)

14. (Mases 1 to 1034)

15. Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

16. Pull-length cDNA libraries and normalization

17. Unpublished (2001)

18. On Feb 15, 2001 this sequence version replaced gi:31275103.

19. Contact: Genoscope

19. Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr

18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster
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AL553289 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
AL553289
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primer="Ist straine end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                      TyrSerArgGlyHisPheAspArgThrLysLysGlyThrSerSerLysLysVallleTyr
                                                                                           GCAGCCGTCCTTGTAACCCTGATTCTCCTGNGAAATCTGGTTTTTGGCATCTGGTTTGCC
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AlaAlaValLeuValThrLeuIleLeuLeuGlyIleLeuValPheGlyIleTrpPheAla
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                can
DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LiML at: http://image.llnl.gov column: 13
Plate: LLCM2662 row: c column: 13
High quality sequence stop: 685.
Location/Qualifiers
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BQ928243 GI:22343274
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Bukaryofta.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (basea I to 94).

I (basea I to 94).

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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25-normalized
                                                                                                                                                                                                                                                                                    Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                       AlaAlaValLeuValThrLeuIleLeuLeuGlyIleLeuValPheGlyIleTrpPheAla 260
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Catarrhini; Hominidae; Homo.
                                      CGTGCCTTCAGCAACTCTTCCTATGTCCTGAATCCCACAACAGGAGAGCTGGTCTTTGAT
                                                                                                                                                                                                                              GCAGCCGTCCTTGTAACCCTGNNATCTCTGTGNGAATCTTGGTTTTTGGCATCTGGTTTTGCC
                                                                                                                     ProMetThrSerAsnAlaValArgMetGluAlaValGluArgAsnValGlyValIleVal
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (bases 1 to 1488)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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/db_xref="taxon:9606"
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CR608619
CR608619.1 GI:50489426
HTC; CNSLT cDNA.
HOMO sapiens (human)
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mRNA linear EST 21-AUG-2002 sapiens cDNA clone IMAGE:6480623
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 886)

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                       157 TIGICCCCTGGCATIGGGCAGTGTTACAGTGCACTCTTCTGAACCTGAAGTCAGAATT
                                                                                                                             CCTGAGAATAATCCTGTGAGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTG
                                                                                                                                                                                                                               AlaSerTyrGluAspArgValThrPheLeuProThrGlyIleThrPheLysSerValThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTGCCTTCAGCAACTCTTCCTATGTCCTGAATCCCACAACAGGAGAGCTGGTCTTTGAT
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                                                                                          41 ProGludsnAsnProValLysLeuSerCysAlaTyrSerGlyPheSerSerProArgVal
                                                                                                                                                                                                  GluTrpLysPheAspGlnGlyAspThrThrArgLeuValCysTyrAsnAsnLysIleThr
                                                                                                                                                                                                                                                                                                                                       GCTTCCTATGAGGACCGGGTGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACA
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LeuCysSerLeuAlaLeuGlySerValThrValHisSerSerGluProGluValArgile
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AUTHORS
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777

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Genoscope - Centrer National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequeréfégenoscope.cns.fr. Web : www.genoscope.cns.fr. yeb interest. Sequence cope.cns.fr. Web interest. Sequence cope.cns.fr. web interest. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B96 bp mRNA linear EST 27-APR-2004 BX379273 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA CLONE CSODI032YK05 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                        AlaAlaValLeuValThrLeuIleLeuLeuGlyIleLeuValPheGlyIleTrpPheAla 260
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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1 (bases 1 to 80 pt.

11, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

On May 8, 2003 this sequence version replaced gi:30456760.

Contact: Genoscope
                         ArgAlaPheSerAsnSerSerTyrValLeuAsnProThrThrGlyGluLeuValPheAsp
                                                                                                                                          ProLeuSerAlaSerAspThrGlyGluTyrSerCysGluAlaArgAsnGlyTyrGlyThr
                                                                                                                                                                                                                                      CCCCTGTCAGCCTCTGATACTGGAGAATACAGCTGTGAGGCACGGAATGGGTATGGGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TyrSerArgGlyHisPheAspArgThrLys-LysGlyThrSer 274
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Conservative:
Mismatches:
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1032YK05"
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/tissue type="carcinoma, cell line"
/tissue type="carcinoma, cell line"
/lab_hofe="MHIOB (phage-resistant)"
/clone lib="NHH MGC 40"
/note="organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluValLysValLysLeuIleValLeuValProProSerLysProThrValAsnIlePro 140
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Upublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapberr@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Pitch://image.llnl.gov
Plate: LLCM2660 row: k column: 24
High quallity sequence stop: 698.
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Matches:
                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="carcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clome_lib="NIH_MGC Libers"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
/note="Organ: prostate; Vector: potB7; Vector: potB7;
                                                                                            Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I:M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I:M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2660 row: c column: 15

High quality sequence stop: 692.
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  1 (bases 1 to 907)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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AGENCOURT 10039280 NIH_MGC_40 Homo 5', mRNA Eequence.

BQ928239 G1:22343270
                                                                         US-10-785-220B-1 (1-299) x BX379273 (1-896)
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US-10-785-220B-1 (1-299) x BU542115
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85.10%
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DB:
                  Percent Similarity:
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BU542115 GI:22852598
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                                                                                                     AlaAlaValLeuValThrLeuIleLeuLeuGlyIle-LeuValPheGlyIleTrpPheAl 260
                                                                                                                              260 a---TyrSerArgGlyHia-PheAspArgThrLys---LysGlyThrSerSerLysLys 277
                                                                                                                                                        CCTTCTGAATACACCTGGTTCAAAGATGGGATAGTGATGCCTACGAATCCCCAAAAGCACC
                                                                    ProLeuSerAlaSerAspThrGlyGluTyrSerCysGluAlaArgAsnGlyTyrGlyThr
ProSerGluTyrThrTrpPheLysAspGlyIleValMetProThrAsnProLysSerThr
                                                                                  CCCCTGTCAGCCTCTGATACTGGAGAATACAGCTGTGAGGCACGGAATGGGTATGGGACA
                                                                                               ProMetThrSerAsnAlaValArgMetGluAlaValGluArgAsnValGlyValIleVal
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       481
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1039 bp mRNA linear EST 29-MAR-2002
AGENCOURT 6924454 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5813758
5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                             351 CGGGAAGACACTGGGACATACACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluValLysValLysLeulleValLeuValLeuValProProSerLysProThrValAsnIlePro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          771 GGCAGCCGTCCTTGTAACCCTGATTCTCCTGGGAAATCTTGGTTTTTGGGCATCTGGTTT
                                                                                                                                                                              LeuCysSerLeuAlaLeuGlySerValThrValHisSerSerGluProGluValArgIle
                                                                                                                                                                                                                                                                                             GluTrpLysPheAspGlnGlyAspThrThrArgLeuValCysTyrAsnAsnLysIleThr
                                                                                                                                                                                                                                                                                                                                                                                                            101 ArgGluAspThrGlyThrTyrThrCysMetValSerGluGluGlyGlyAsnSerTyrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProMetThrSerAsnAlaValArgMetGluAlaValGluArgAsn-ValGlyValIleVa
                                                                                                                          MetGlyThrLysAlaGlnValGluArgLysLeuLeuCysLeuPhelleLeuAlaIleLeu
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267
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                           Conservative:
Mismatches:
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Length:
Matches:
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798

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CD384890 891 bp mRNA linear EST 30-MAY-2003
AGENCOURT 14286171 NIH_MGC_173 Homo sapiens CDNA 5', mRNA sequence.
CD384890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 -PheAlaTyrSerArg-GlyHisPheAspArgThr-LysLysGlyThr-SerSer---Ly 276
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Cancer S. Gerhard, Ph.D.
Office of Cancer Institute / NIH
Bldg. 31 RmloAn7 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jamie Thompson, University of WI
Tissue Procurement: Dr. Jamie Thompson, University of WI
CDNA Library Preparation: Gina Zastrow-Hayes
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                     CCCCTGTCAGCCTCTGATACTGGAGAATACAGCTGTGAGGCACGGAATGGGTATGGGACA
                                                              GAGGICAAGGICAAGCICATCGIGCTIGIGCCICCATCCAAGCCIACAGTIAACAICCCC
                                                                                                                                                                                                       CCTTCTGAATACACCTGGTTCAAAGATGGGATAGTGATGCCTACGAATCCCCAAAAGCACC
                                                                                                                                                                                                                                                                                      CGTGCCTTCAGCAACTCTTCCTATGTCCTGAATCCCACAACAGGAGAGCTGGTCTTTGAT
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                                                                                                                                             TCCTCTGCCACCATTGGGAACCGGGCAGTGCTGACATGCTCAGAACAAGATGGTTCCCCA
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                        GluValLysValLysLeuIleValLeuValProProSerLysProThrValAsnIlePro
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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High quality sequence stop: 703.
Location/Qualifiers
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                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 1039)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                               Email: cgapD8-remail.nih.gov
Tissue Procurement: Low Standt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Flate: LLCM2066 row: e column: 23
High quality sequence stop: 716.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTTCCTATGAGGACCGGGTGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 LeuCysSerLeuAlaLeuGlySerValThrValHisSerSerGluProGluValArgIle
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1309.50
90.94%
89.32%
84.81%
                        sapiens
                                             Homo sapiens
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KEYWORDS
SOURCE
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                                                                                                                    AUTHORS
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/tissue_type="carcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_40"
/clone_lib="NIH MGC_40"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Bite_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                              BQ887533 878 bp mRNA linear EST 16-AUG-2002
AGENCOURT 8675238 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6380256
5, mRNA sequence.
BQ887533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ATGGGGACAAAGGCGCAAGTCGAGAGAAACTGTTGTGCCTCTTCATATTGGCGATCCTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: LLCM2568 row: j column: 01
High quality sequence stop: 614.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 878)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               878
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                                     854 TTGGCCTATAGGCCGAGGGCACTT
                 259 -PheAlaTyrSerArgGlyHisPhe
                                                                                                                                                                                                         BQ887533.1 GI:22279547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.56e-129
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82.97%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaSerTyrGluAspArgValThrPheLeuProThrGlyIleThrPheLysSerValThr 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314 GCTTCCTATGAGGACCGGGTGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ArgGluAspThrGlyThrTyrThrCysMetValSerGluGluGlyGlyAsnSerTyrGly 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 CGGGAAGACACTGGGACATACATTGTATGGTCTCTGAGGAAGGCGGCAACACAGCTATGG 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluTrpLysPheAspGlnGlyAspThrThrArgLeuValCysTyrAsnAsnLysIleThr 80
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LIBR_PRIMING - oligo dT; METHÖD - full-length enriched;
LIBR_PROVIDER - Bradfield"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             494 TCCTCTGCCACCATTGGGAACCGGGCAGTGCTGACATGCTCAGAACAAGATGGTTCCCCA
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                                                       WA01
                                                       from
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                                                                                                                                                                                                                                                891
1262
133
155
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Matches:
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organism="Homo sapiens"
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AsnLysileThr 	ysservalThi                  \AGTCCGTGACZ	AsnSerTyrGly             \aCAGCTATGGG	/alasnilePro                sttaaCatcCcc	AspGlySerPro                3ATGGTTCCCC	rolysserth             ccaaaagcacc	yGluLeuValPheAsp                   AGAGCTGGTCTTTGAT	slytyrglythr             sggtatgggaCa	/alGlyvalIle     GGGGGTCATCC	phe-GlylleTr              TTGGCATCTG	
alCysTyrAsnA               TTGCTATAATA	SlyileThrPhe	rThrCysMetValSerGluGluGlyGlyAsnSerTh 	erLysProThr              CCAAGCCTACA	ysserglugln            GCTCAGAACAA	let ProThrasn            \TGCCTACGAAT	hrThrGlyGlu             CAACAGGAGAG	ilualaargasn            iaggcacggaat	lluargasn'        agccgcaatco	IleLeuVal      AATCTTGGGTT	
hrThrArgLeuVal 	heLeuProThr(            rcTTGCCAACTC	ysMetValSer( 	euValProPro6             TTGTGCCTCCA1	laValLeuThrd            CAGTGCTGACA1	spGlylleValN                ATGGGATAGTG1	yrValLeuAsnProThrThrGl 	luTyrSerCys(                AATACAGCTGTC	etGluAlaValC             rGGAAGCTGTGC	eLeuLeuGly-            TCTCCTGGGG/	heAsparg 268   :::::  TGAACAG 873
pGlnGlyAspTh             CCAAGGAGACAC	pArgValThrP              CCGGGTGACCT	YThrTyrThrC                  GACATACACTT	BLeulleValL               GCTCATCGTGC	eGlyAsnArgA             'TGGGAACCGGG	rTrpPheLysA              CTGGTTCAAAG	nSerSerTyrV              CTCTTCCTATG	raspThrGlyG              TGATACTGGAG	nAlavalArgM             TGCTGTGCGCA	uValThrLeuI             TGTAACCTGA	Arg-GlyHisP             CGAGGGCCACT
GlutrpiysPheAspGlnGlyAspThrThrArgLeuValCysTyrAsnAsnIysIleThr 	AlaSerTyrGluAspArgValThrPheLeuProThrGlylleThrPheLysSerValThr 	ArggluaspthrGlythrTyrThrCysMetValSerGluGluGluGlyGlyasnSerTyrGly 	GluvaliysvaliysLeuileValiceuValProProSeriysProThrValAsnilePro 	SerSerAlaThr11eGlyAsnArgAlaValLeuThrCysSerGluGlnAspGlySerPro 	ProSerGluTyrThrTrpPhelysAspGlylleValMetProThrAsnProlysSerThr 	ArgalaPheSerasnSerSerTyrValLeuasnProThrThrGlyGluLeuValPheAsp 	ProLeuSerAlaSerAspThrG1yG1uTyrSerCysG1uAlaArgAsnG1yTyrG1yThr 	PrometThrSerasnalavalargmetGlualavalGluargasnvalGlyvalIle 	ValAlaAlaValLeuValThrLeuIleLeuLeuGlyIleLeuValPhe-GlylleTr 	p-PheAlaTyrSerArg-GlyHisPheAspArg                     GGTTTGCCTATAGCCGAGGGCCACTTTGAACAG
61 G1 	81 Al    301 GC	101 Ar    361 CG	121 Gl    421 GA	141 Se 	161 Pr    541 CC	181 Ar    601 CG	201 Pr    661 CC	221 Pr     21 CC	240 Va 781 TG	258 p- 841 GG
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